

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 19:42:38 ; Search time 5782 Seconds
(without alignments)
3964.917 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
Sequence: 1 MDLRILFGPTCTGKTSTAIA.....KPLVGAATVAEAFEGPPFRM 239

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 636136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1230	100.0	1919	2	CQ895587
2	1230	100.0	1919	15	ABTIPT
3	1230	100.0	2722	2	AX039930

4	1230	100.0	2722	2	AX039931	AX039931 Sequence
5	1230	100.0	3017	2	AX039934	AX039934 Sequence
6	1230	100.0	5622	2	AX039929	AX039929 Sequence
7	1075	87.4	723	2	CQ899250	CQ899250 Sequence
8	1075	87.4	1983	15	ATTMRPTI	X00639 Agrobacteri
9	1075	87.4	9931	15	AE007927	AE007927 Agrobacte
10	1075	87.4	10377	15	AE009419	AE009419 Agrobacte
11	1075	87.4	206479	15	AB016260	AB016260 Agrobacte
12	1066	86.7	29524	15	ATU237588	AJ237588 Agrobacte
13	1052	85.5	1997	15	AB025109	AB025109 Agrobacte
14	1050	85.4	1382	15	PLATITPTG	X17428 Plasmid Ti
15	1050	85.4	10200	15	ATTAAAH	X56185 A. tumefacie
16	1050	85.4	14960	15	AVU83986	U83986 Agrobacteri
17	1050	85.4	15463	15	AVU83987	U83987 Agrobacteri
18	1035	84.1	2724	15	AB032122	AB032122 Agrobacte
19	1005	81.7	723	2	AR564460	AR564460 Sequence
20	1005	81.7	1296	15	TIIPMR	K02000 Ti plasmid
21	1005	81.7	24595	2	BD016312	X00010 Agrobacteri
22	1005	81.7	24595	2	E00406	BD016312 Method of
23	1005	81.7	24595	2	E00546	E00404 Ti Plasmid
24	1005	81.7	24595	2	E00546	E00546 DNA Fragment
25	1005	81.7	24595	2	AR364803	AR364803 Sequence
26	1005	81.7	24595	15	ATACHS	X00493 Agrobacteri
27	1005	81.7	194140	15	AF242881	AF242881 Agrobacte
28	995	80.9	3182	2	AR201516	AR201516 Sequence
29	994	80.8	747	2	AR564455	AR564455 Sequence
30	993	80.7	6482	15	AVIAAM	X73327 A. vitis 1aa
31	984	80.0	3183	2	I75096	I75096 Sequence 1
32	686.5	55.8	2544	2	AR564457	AR564457 Sequence
33	614	48.9	3271	15	TS4IPTVT	X01610 Plasmid PTi
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35	605.5	49.2	1413	15	ATTZS	X02423 Agrobacteri
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41	603.5	49.1	12802	15	TIIPREGU	U03320 Plasmid Ti
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ALIGNMENTS

RESULT 1
LOCUS CQ895587 1919 bp DNA linear PAT 05-NOV-2004
DEFINITION Sequence 1 from Patent WO2004090143.
ACCESSION CQ895587
VERSION CQ895587.1 GI:55467720

SOURCE

ORGANISM Agrobacterium tumefaciens (Rhizobium radiobacter)
Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.

REFERENCE

AUTHORS Habben, J.F., Zinselmeier, C., Tomez, D.T., Abdlitt, S.E.,
Helentjaris, T.G. and Niu, X.
TITLE Modulation of cytokinin activity in plants
JOURNAL Patent: WO 2004090143-A 1 21-OCT-2004;
PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES

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ORIGIN

Alignment Scores:

Pred. No.:	1,976-126	Length:	1919
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-817-483-2 (1-239) x CO895587 (1-1919)

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Qy	21	LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln	40
Db	750	CTTGCCCAAGACAGCTGGCTCCCAAGTCTCTCGCTCGATCGGCTCAATGCTGCTCAA	809
Qy	41	LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr	60
Db	810	CTATCAACCGGAAGCGGCGACCAACAGTGAAGAACGAAAGAACACACTCGCTGTAC	869
Qy	61	LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu	80
Db	870	CTTGATGATCGCCCTTTGGTAAAGGATATCATTTACGCCAACCAAGCTCATGAACGGCTC	929
Qy	81	IleAlaGluValHisAsnHisGlnAlaLysGlyLeuIleLeuGluGlyGlySerIle	100
Db	930	ATTGGGAGGTGCACAAATCAGAGGCCAAAGCGGGCTTATTCTTGAGGAGGATCTATC	989
Qy	101	SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle	120
Db	990	TCGTTGCTCAGGTGCATGGCGCAAGTCGTTATGGAACGGCGATTTTCGTTGGCATATT	1049
Qy	121	IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys	140
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Db	1230	GCTACCCGAAACGAGATCACGCCCGATATGCTATTGCGAGCTGCAGCCGAGATGAGAAAT	1289
Qy	201	LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys	220
Db	1290	AAATGATTCACGGGATCGCTCAGAGTTTCTTAATCCATCGCGCTCGACAGGAACAGAAA	1349
Qy	221	PheProLeuValGlyAlaThrAlaValGlnAlaPheGluGlyProProPheArgMet	239
Db	1350	TYCCCTTGTGGGCGACAGCTGTCAAGGCTTGAAGACCACTTTCGATG	1406

RESULT 2

ABTIPT	1919 bp	DNA	linear	BCT 12-SEP-1993
LOCUS	ABTIPT	Agrobacterium tumefaciens Ti plasmid ipt gene for isopentenyl		
DEFINITION	transferrase.			
ACCESSION	X14410	X17432		
VERSION	X14410.1	GI:38689		

KEYWORDS

ipt gene; isopentenyl transferase; transferase.
Agrobacterium tumefaciens (Rhizobium radiobacter)

SOURCE

Agrobacterium tumefaciens (Rhizobium radiobacter)

ORGANISM

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

REFERENCE

Rhizobiaceae; Agrobacterium.

AUTHORS

1 (bases 1 to 1919)

TITLE

Strabala, T.J., Bednarek, S.Y., Bertoni, G. and Amsino, R.M.

JOURNAL

Isolation and characterization of an ipt gene from the Ti plasmid

PUBMED

B0542

REFERENCE

Mol. Gen. Genet. 216 (2-3), 388-394 (1989)

AUTHORS

2 (bases 1 to 1919)

TITLE

Strabala, T.

JOURNAL

Direct Submission

FEATURES

Submitted (02-FEB-1989) Strabala T., Department of Biochemistry,

source

University of Wisconsin Madison, 420 Henry Mall, Madison WI 53706

FEATURES

Location/Qualifiers

source

1..1919

CDS

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FEATURES

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/plasmid="Ti"

FEATURES

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FEATURES

/note="unnamed protein product; isopentenyl transferase

FEATURES

(AA 1-239)"

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FEATURES

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ORIGIN

Alignment Scores:

Pred. No.:	1,976-126	Length:	1919
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	15	Gaps:	0

US-10-817-483-2 (1-239) x ABTIPT (1-1919)

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Qy	21	LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln	40
Db	750	CTTGCCCAAGACAGCTGGCTCCCAAGTCTCTCGCTCGATCCGCTCAATGCTGCTCAA	809
Qy	41	LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr	60
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Qy	61	LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu	80
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Qy	81	IleAlaGluValHisAsnHisGlnAlaLysGlyLeuIleLeuGluGlyGlySerIle	100
Db	930	ATTGGGAGGTGCACAAATCAGAGGCCAAAGCGGGCTTATTCTTGAGGAGGATCTATC	989
Qy	101	SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle	120
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Qy	121	IIleArgSngIuLeuAlaAspGluGluSerPheMetSerValAlaIleThrArgValIys	140
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Qy	141	GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg	160
Db	1110	CAGATGTTACGCCCTCTGCAGAGCTTTCTATTATCCAAAGTTGGTTCAACTTTGGAGG	1169
Qy	161	GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe	180
Db	1170	GAGCTCGGCTGAGAGGCCCATCTGGAAGGATCGATGATATCGATATAGCCCTGTAATT	1229
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Db	1230	GCTACCCAGAAACCGATCACGCCCGGATGTCTATTGTCAGCTCGACGCGAGATATGAGAAAT	1289
Qy	201	LeuLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGluIleIys	220
Db	1290	AAATTTGATTCACGGTATTCGCTCAGAGAGTTCTTAATCCATGGCGGTCCACAGAAACAGAAA	1349
Qy	221	PheProLeuValGlyAlaThrAlaValGlnAlaPheGluGlyProProPheArgMet	239
Db	1350	TTCCCTTTGGTGGGCGACAGCTGTGCAACGCTTTGAAGAACCAACCATTTTCGAATG	1406

RESULT 3				
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LOCUS	AX039930	2722 bp	DNA	linear
DEFINITION	Sequence 8 from Patent WO0063401.			
ACCESSION	AX039930			
VERSION	AX039930.1	GI:11229959		
KEYWORDS				
SOURCE				
ORGANISM	synthetic construct			
	synthetic construct			
	other sequences; artificial sequences.			

AUTHORS	Habben, J. E., Zinselmeier, C. and Tomes, D.
TITLE	Regulated expression of genes in plant seeds
JOURNAL	Patent: WO 0063401-A 8 26-OCT-2000;
FEATURES	PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Pred. No.:	3,23e-126
Score:	1230.00
Percent Similarity:	100.0%
Best local Similarity:	100.0%
Query Match:	100.0%
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DS-10-817-483-2 (1-239)	x AX039930 (1-2722)

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41	1645		
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60	1704		

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Qy	81	ILeAlaGluaValHISaenHISgluaAlaIySGlyLeuIleuengIugIySerIle	100
Db	1765	ATTGCGAAGGTGCACATCAAGAGGCCAAAGGGCGGCTTATTTCTTGAGGGAGATTCATTC	1824
Qy	101	SerIeuleuArGySwetAlaGlnSerArGyTTPaSnAlaasPheArGTpHisIle	120
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Qy	161	GluProArGLeuArGProIleLeuGluGlyIleasPGLyTyrArGlyraIaLeuLeuPhe	180
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Qy	221	PheProIeuaValGlyAlaThrAlaValaValAlaPheGluGlyProProPheArGMet	239
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DEFINITION	Sequence 9 from Patent WO0063401.
ACCESSION	AX039931
VERSION	AX039931.1 GI:11229960
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 Haben,J.E., Zinsmeister,C. and Tomes,D.
TITLE	Regulated expression of genes in plant seeds
JOURNAL	Patent: WO 0063401-A 9 26-OCT-2000;
	PIONEER HI-BRED INTERNATIONAL, INC. (US)

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and General Genetics 216:388-394 (1989); terminator from
Solanum tuberosum, Plant Cell 1(1):115-122 (1989)."
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ORIGIN		
Alignment Scores:		
Pred. No.:	3.23e-126	Length: 2722
Score:	1230.00	Matches: 239
Percent Similarity:	100.0%	Conservative: 0
Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	100.0%	Indels: 0
DB:	2	Gaps: 0
US-10-817-483-2 (1-239)	x AK039931 (1-2722)	

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Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
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Db 1765 ATTCGGAGGATGACCAATCACAGAGCCAAAGCGGGCTTATTTCTTGAAGAGATCTATC 1824
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Qy 121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaLysThrArgValLys 140
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Qy 161 GluProArgLeuArgProIleLeuGlnGlyLleAspGlyTyrArgTyrAlaLeuLeuPhe 180
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Db 2125 AAATTGATTCACGGATATGCTCAGAGATTCTTAATCCATGCGCGTCGACAGAAACAGAA 2184
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RESULT 5
AX039934 3017 bp DNA linear PAT 18-NOV-2000
LOCUS AX039934
DEFINITION Sequence 12 from Patent WO0063401.
ACCESSION AX039934.1 GI:11229963
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Habben,J.E., Zinselmeier,C. and Tomes,D.
AUTHORS Regulated expression of genes in plant seeds
TITLE Patent: WO 0063401-A 12-26-OCT-2000;
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers
source
1..3017
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Promoter from Zea mays, Genbank Accession #U22344;
Gene from Agrobacterium tumefaciens, Molecular and General
Genetics 216:388-394 (1989); terminator from Zea mays,
Genbank Accession #U22345."

ORIGIN

Alignment Scores:
Pred. No.: 3 73e-126 Length: 3017
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-817-483-2 (1-239) x AX039934 (1-3017)

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Qy 21 LeuA1aGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 1468 CTTGCCGACGACATGGGCTCCGACTCTCTCGCTCGATCCGCTCCATGCTGCTCTCA 1527
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
Db 1528 CTATCAACCGGAGCGGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTGCTGTGAC 1587
Qy 61 LeuAspAspArgProLeuValLysGlyLleIleThrAlaLysGlnAlaHisGlnuArgLeu 80
Db 1588 CTTGATGATCGCCCTTTGGTAAAGGATATCATTTACAGCCAAAGCAAGCTCATGAAAGGCTC 1647
Qy 81 IleA1aGlnValHisAsnHisGlnuAlaLysGlyLeuLleLeuGlnGlyLysSerIle 100
Db 1648 ATTCGGAGGATGACCAATCACAGAGCCAAAGCGGGCTTATTTCTTGAAGAGATCTATC 1707
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTriPheAlaAspPheArgTriPheIle 120
Db 1708 TCGTTGCTCAGAGTGCATGCGCAAGTGTATTTGGAACGGGATTTTCGTTGGCATATT 1767
Qy 121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaLysThrArgValLys 140
Db 1768 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCAAACAGAGCTTAAG 1827
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTriParg 160
Db 1828 CAGATGTATACGCCCTCTGCAAGGTCTTCTATTATCCAAAGATTGTTCACTTTGGAGG 1887
Qy 161 GluProArgLeuArgProIleLeuGlnGlyLleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 1888 GAGCTTCGGCTGAGGCGCCATCTGAGAGGATCGATGATTCGATATGCTCTGCTATT 1947
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
Db 1948 GCTACCCGAAACAGATACGCCCGCATATGCTATTGCAAGCTCGACGACGATATGAGAAAT 2007
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
Db 2008 AAATTGATTCACGGATATGCTCAGAGATTCTTAATCCATGCGCGTCGACAGAAACAGAA 2067
Qy 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
Db 2068 TTCCCTTGTGTGGGCGCAGAGCTGTGAAAGCGTTTGAAGACCACTTTTCGAATG 2124

RESULT 6
AX039929 5622 bp DNA linear PAT 18-NOV-2000
LOCUS AX039929
DEFINITION Sequence 7 from Patent WO0063401.
ACCESSION AX039929
VERSION AX039929.1 GI:11229958
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Habben,J.E., Zinselmeier,C. and Tomes,D.
AUTHORS Regulated expression of genes in plant seeds
TITLE Patent: WO 0063401-A 7-26-OCT-2000;
JOURNAL PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES
source
Location/Qualifiers
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/organism="synthetic construct"
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Genbank, Accession #S78780; gene from Agrobacterium
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216:388-394 (1989)."

ORIGIN
Alignment Scores:
Pred. No.: 8,99e-126 Length: 5622
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-817-483-2 (1-239) x AX039929 (1-5622)

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QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 1585 CTTGCCACAGACAGCTCCCTCCAGTCCCTCGCTCGATCGCGTCCAAATGCTGCTCA 1644
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLeuGlyThrThrArgLeuThr 60
DB 1645 CTATCAACCGGAAGCGGCGGACCAACAGTGAAGAACTGAAGAAACGACTGCTGATC 1704
QY 61 LeuAspAspArgProLeuValLeuGlyGlyIleIleThrAlaLeuGlnAlaHisGlnArgLeu 80
DB 1705 CTTGATGATCGCCCTTTGGTAAAGGATCATTCACGCCAACCAAGCTCATAGACGGCTC 1764
QY 81 IleAlaGlnValAlaHisAsnHisGlnAlaLeuGlyGlyLeuIleLeuGlnGlyGlySerIle 100
DB 1765 ATTCGAGAGTGCACATCATCAGAGCGCAAGCGGGCTTATCTTGAGGAGGATCTATC 1824
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DB 1825 TCGTTGCTCAGGTGATGCGCAAGTCTTATTCAGAACGCGATTTTCGTTGGCATATT 1884
QY 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaLeuThrArgValLeu 140
DB 1885 ATTCGACAGAGTATGACAGACAGAGAGAGCTTCATAGCGTGGCCAAAGCCAGATTAAG 1944
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuThrArg 160
DB 1945 CAGATGTTACGCCCTCTGTCAGATCTTCTATTATTCAGAGATGGTTCATCTTGAGAGG 2004
QY 161 GlnProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 2005 GAGCCTCGGCTAGAGCCCATCTACTGAAAGGATCGATGATATCGATATCCCTGCTATT 2064
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
DB 2065 GCTACCCAGAACCAATCATCGCCCATATGCTATGCTGACACTGCAGACAGATTTGAGAA 2124
QY 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLeu 220
DB 2125 AAATTGATTCACGATATCGCTCAGAGATTCTTATTCATCATGCGCGTGCACAGAAACGAAA 2184
QY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB 2185 TTCCTTTGGTGGGCGACAGCTGTGGAAGCGTTGAAGACCAACATTTTGAATG 2241

RESULT 7
CQ899250 723 bp DNA linear PAT 08-NOV-2004
LOCUS CQ899250
DEFINITION Sequence 2 from Patent WO2004092390.

ACCESSION CQ899250
VERSION CQ899250.1 GI:55583090
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
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Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 2 Gaps: 0

US-10-817-483-2 (1-239) x CQ899250 (1-723)

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DB 61 CTTGCCACAGACAGCTCCCTCCAGTCCCTCGCTCGATCGCGTCCAAATGCTGCTCA 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLeuGlyThrThrArgLeuThr 60
DB 121 CTTGATGATCGCCCTCTGTCAGATCTTCTATTATTCAGAACGCGATTTTCGTTGGCATATT 180
QY 61 LeuAspAspArgProLeuValLeuGlyGlyIleIleThrAlaLeuGlnAlaHisGlnArgLeu 80
DB 181 CTTGATGATCGCCCTCTGTCAGATCTTCTATTATTCAGAACGCGATTTTCGTTGGCATATT 240
QY 81 IleAlaGlnValAlaHisAsnHisGlnAlaLeuGlyGlyLeuIleLeuGlnGlyGlySerIle 100
DB 241 ATGGGAGAGTGTATATATATATGAGGCCACAGCGGGCTTATTTCTGAGGAGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgIleIleThrAlaLeuGlnAlaHisGlnArgLeu 120
DB 301 TCGTTGCTCAGTGTGATGCGCAAGCATTAATGAGATGGGATTTTCGTTGGCATATT 360
QY 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaLeuThrArgValLeu 140
DB 361 ATTCGACAGAGTATGACAGACAGACAGACAGATTCATGAAAGCTGCGCAAGCCAGATTAAG 420
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DB 421 CAGATGTTACGCCCTCTGTCAGATCTTCTATTATTCAGAGATGGTTCATCTTGAGAA 480
QY 161 GlnProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCCTCGGCTAGAGCCCATCTACTGAAAGATCGATGATATCGATATCCATGTTGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
DB 541 GCTACCCAGAACCAATCATCGCCCATATGCTATGCTGACACTGCAGACAGATTTGAGAA 600
QY 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLeu 220
DB 601 AAGTTGATTCATGAGATCGCTCAGAGATATCTCATTCATCGCCGACCAAGAACGAAA 660

OY 221 PheProLeuVal1g1yAla1ThrAla1Val1Glu1Ala1Phe1Glu1Gly1Pro1ProPheArgMet 239
DB 661 TTCCTCGAGTTAAGCAGCGCGCTTAAGCATTCATTCATTCGATG 717

RESULT 8
ATTMRPT1 1983 bp DNA linear BCT 18-APR-2005
DEFINITION Agrobacterium tumefaciens pTiT37 T-DNA tmr locus.
ACCESSION X00639.1 GI:944822
VERSION X00639.1 GI:944822
KEYWORDS cyclokinin; plasmid.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens (Rhizobium radiobacter); Rhizobiales;
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.

REFERENCE
1 (bases 1 to 1982)
AUTHORS Goldberg, S.B., Flick, J.S. and Rogers, S.G.
TITLE Nucleotide sequence of the tmr locus of Agrobacterium tumefaciens
pTi T37 T-DNA
JOURNAL Nucleic Acids Res. 12 (11), 4665-4677 (1984)
COMMENT PubMed
FEATURES
source
On Aug 15, 1995 this sequence version replaced gi:39174.
Location/Qualifiers
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CAAT_signal 545..553
TATA_signal 588..592
CDS 659..1381
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ORIGIN
polyA_signal 1418..1422

Alignment Scores:
Pred. No.: 3,81e-109 Length: 1983
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 15 Gaps: 0

US-10-817-483-2 (1-239) x ATTMRPT1 (1-1983)

OY 1 MetAspLeuArgLeu1IlePheGlyPro1ThrCys1ThrGly1Ys1ThrSer1ThrAla1IleAla 20
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OY 21 LeuAlaGlnGln1ThrGly1LeuProVal1LeuSer1LeuAspArgVal1GlnCys1Cys1ProGln 40
DB 719 CTGGCCAGCAGACGTGGCTTCCTTCGCTCGATCGGGTCCAAATGTTGCTCTAG 778

OY 41 LeuSer1ThrGly1SerGly1ArgPro1ThrVal1GluGluLeu1Ys1Gly1Thr1Arg1Leu1Yr 60
DB 779 CTGTCAACCGAAGCGAGACGACCAACATGTGAAAGAAACAGACCGCTTATAC 838

OY 61 LeuAspAspArgPro1LeuVal1Ys1Gly1Ile1ThrAla1Ys1GlnAla1His1Glu1ArgLeu 80
DB 839 CTTGATGATCGGCTCTGCTGTAAGGGTATCATTCGACCAAGCATCATGAAAGGCTG 898

OY 81 IleAlaGluVal1HisAsnHis1GlnAla1Ys1Gly1Ys1Leu1IleLeu1Glu1Gly1Ser1Ile 100
DB 899 ATGGGAGAGGTGTAATTAATTATAGAGCCACGCGCGGCTTATCTTGAGGGAGATCTATC 958

OY 101 SerLeuLeuArgCysMetAlaGlnSerArg1Yr1TrpAsnAlaAspPheArg1TrpHis1Ile 120
DB 959 TCGTTGCTCAAGTCATCGCGCCAAAGCAGTATTCGAGTGGCATTTTCGTTGGCATATT 1018

OY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerVal1Ala1Ys1ThrArgVal1Ys 140
DB 1019 ATTCGCCACGAGTTAGACGAGAGAGACCTTCATGAACTGGCCAGGCGCAGAGTTAAG 1078

OY 141 GlnMetLeuArgPro1SerAla1GlyLeuSer1Ile1IleGlnGluLeuVal1GlnLeu1TrpArg 160
DB 1079 CAGAGTTACCGCCCTGCTGAGCGGCTTCTATATCCAAAGTTGGTTGATCTTTGGAAA 1138

OY 161 GluProArgLeuArgPro1LeuLeuGluGly1IleAspGly1YrArg1YrAla1LeuLeuPhe 180
DB 1139 GAGCTCGGCTGAGGCGCCATCTGAAAGAGATCGATATGATGATGATGATGATGATGAT 1198

OY 181 AlaThrGlnAsnGln1Ile1ThrPro1AspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
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DB 1259 AAGTTGATTCATGGATGCTCAGAGATATCTTCATTCATGACGCCGACAAAGAACAGAAA 1318

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DB 1319 TTCCTCGAGTTAAGCAGCGCGCTTAAGCATTCATTCATTCGATG 1375

RESULT 9
AE007927 9931 bp DNA linear BCT 28-MAY-2004
LOCUS Agrobacterium tumefaciens str. C58 plasmid T1, section 5 of 20 of
DEFINITION the complete sequence.
ACCESSION AE007927 AE007871
VERSION AE007927.2 GI:16271969
KEYWORDS
SOURCE Agrobacterium tumefaciens str. C58
ORGANISM Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.

REFERENCE
1 (bases 1 to 9931)
Hinkle, G., Slater, S.C. and Goodner, B.
TITLE Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
Disease in Plants
JOURNAL Unpublished
AUTHORS Hinkle, G., Slater, S.C. and Goodner, B.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
Cambridge, MA 02139, USA
COMMENT On Oct 19, 2001 this sequence version replaced gi:15163470.
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gene
CDS

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Alignment Scores:		
Pred. No.:	3 71e-108	length: 9931
Score:	1075.00	Matches: 206
Percent Similarity:	93.7%	Conservative: 18
Best Local Similarity:	86.2%	Mismatches: 15
Query Match:	87.4%	Indels: 0
DB:	15	Gaps: 0
US-10-817-483-2 (1-239)	x AE007927 (1-9931)	

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Db	6176	CTTCCCGACGACGATGGGGCTTCCAGTCTCTTGGTGGATGGGGTCCAAATGTTTGCTCAG	6235
QY	41	LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr	60
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QY	61	LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu	80
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QY	81	IleAlaGluValHisAsnHisGluAlaLysGlyGlyLeuLeuGlnGlyGlySerIle	100
Db	6356	ATGGGGGAGGGTATATATTATGAGGCCACGGCGGGCTTATTTCTTGAGGGAGATCTATC	6415
QY	101	SerLeuLeuArgCysMetAlaGlnSerArgTyrTTrpAsnAlaAspPheArgTrpHisIle	120
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QY	121	IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaLysThrArgValLys	140
Db	6476	ATTGCGACACAGATTAGAGACGAGGAGAACCTTCAATGAACGTGGCCAAAGGCCAAGATTAAAG	6535
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DEFINITION Agrobacterium tumefaciens str. C58 T1 plasmid, section 2 of 21 of
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ACCESSION AE009419 AE008690
VERSION AE009419.1 GI:17744019
KEYWORDS
SOURCE Agrobacterium tumefaciens str. C58
ORGANISM Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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REFERENCE 1 (bases 1 to 10377)
AUTHORS Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,
Chen, Y., Woo, L., Kitchajima, J.P., Okura, V.K., Almeida, N.F., Jr.,
Zhou, Y., Boyee, D., Sr., Chapman, P., Clendenning, J., Deatherage, G.,
Gillet, W., Grant, C., Guenther, D., Kuttyavin, T., Levy, R., Li, M.,
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Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M.,
Krispan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C.,
Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
and Nester, E.W.
The genome of the natural genetic engineer Agrobacterium
tumefaciens C58
Science 294 (5550), 2317-2323 (2001)
11743193
2 (bases 1 to 10377)
JOURNAL Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,
PUBMED Chen, Y., Woo, L., Kitchajima, J.P., Okura, V.K., Almeida, N.F., Jr.,
REFERENCES Zhou, Y., Boyee, D., Sr., Chapman, P., Clendenning, J., Deatherage, G.,
AUTHORS Gillet, W., Grant, C., Guenther, D., Kuttyavin, T., Levy, R., Li, M.,
McClelland, E., Palmieri, A., Raymond, C., Rouse, G.,
Saenphimmachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I.,
Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M.,
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Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V.
and Nester, E.W.
Direct Submission
TITLE Submitted (27-SEP-2001) Department of Microbiology, University of
JOURNAL Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
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ORIGIN

Alignment Scores:
Pred. No.: 3.95e-108 Length: 10377
Score: 1075..00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 15 Gaps: 0

US-10-817-483-2 (1-239) x AEO09419 (1-10377)

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LOCUS			
DEFINITION	Agrobacterium tumefaciens plasmid pTi-SAKURA, complete sequence.		
ACCESSION	AB016260	AB006857	AB006858
VERSION	AB016260.1	GI:6498173	
KEYWORDS	Agrobacterium tumefaciens (Rhizobium radiobacter)		
SOURCE	Agrobacterium tumefaciens		
ORGANISM	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.		
REFERENCE	1 Hattori,Y., Suzuki,K., Uraji,M., Ohta,N., Katoh,A. and Yoshida,K.		
AUTHORS	Genome structure of pTi-SAKURA (I): strategy for DNA sequencing of		
TITLE	A Japanese cherry-Ti plasmid		
JOURNAL	Nucleic Acids Symp. Ser. 37, 159-160 (1997)		
PUBMED	9586048		
REFERENCE	2 Hattori,Y., Suzuki,K., Ohta,N., Uraji,M., Katoh,A. and Yoshida,K.		
AUTHORS	Genome structure of pTi-SAKURA (V): Complete nucleotide sequence of		
TITLE	plasmid pTi-SAKURA's vir region in Agrobacterium tumefaciens		
JOURNAL	Nucleic Acids Symp. Ser. 39, 265-266 (1998)		
PUBMED	9586048		
REFERENCE	3 Ohta,N., Suzuki,K., Hattori,Y., Uraji,M., Katoh,A. and Yoshida,K.		
AUTHORS	Genome structure of pTi-SAKURA (III): Characteristics of T-DNA		
TITLE	Nucleic Acids Symp. Ser. 39, 185-186 (1998)		
JOURNAL	Nucleic Acids Symp. Ser. 39, 185-186 (1998)		
PUBMED	9586048		
REFERENCE	4 Uraji,M., Suzuki,K., Ohta,N., Hattori,Y., Katoh,A. and Yoshida,K.		
AUTHORS	Genome structure of pTi-SAKURA (IV): Characteristics of tra region		
TITLE	Nucleic Acids Symp. Ser. 39, 187-188 (1998)		
JOURNAL	Nucleic Acids Symp. Ser. 39, 187-188 (1998)		
PUBMED	9586048		
REFERENCE	5 Suzuki,K., Ohta,N., Hattori,Y., Uraji,M., Kato,A. and Yoshida,K.		
AUTHORS	Novel structural difference between nopaline- and octopline-type		
TITLE	trbD genes: construction of genetic and physical map and sequencing		
JOURNAL	of trbD/trai and rep gene clusters of a new Ti plasmid pTi-SAKURA		
PUBMED	Biotech. Biophys. Acta 1396 (1), 1-7 (1998)		
REFERENCE	6 Suzuki,K., Hattori,Y., Uraji,M., Ohta,N., Iwata,K., Murata,K.,		
AUTHORS	Kato,A. and Yoshida,K.		
TITLE	Complete nucleotide sequence of a plant tumor-inducing Ti plasmid		
JOURNAL	Gene 242 (1-2), 331-336 (2000)		

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PUBMED 10721727
REFERENCE 7 (bases 1 to 206479)
AUTHORS Suzuki, K. and Yoshida, K.
TITLE Direct Submission
JOURNAL Submitted (22-JUL-1998) Kazuo Yoshida, Hiroshima University,
Faculty of Science, Kagamiyama 1-3-1, Higashihiroshima-shi,
Hiroshima 735, Japan (E-mail:ksuzuki@ipc.hiroshima-u.ac.jp,
Tel:0824-24-7456, Fax:0824-24-0733)
On or before May 14, 2001 this sequence version replaced
gi:2982699, gi:2982703.

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Alignment Scores:
Pred. No.: 1.74e-106 Length: 29524
Score: 1066.00 Matches: 205
Percent Similarity: 93.34 Conservative: 18
Best Local Similarity: 85.88 Mismatches: 16
Query Match: 86.78 Indels: 0
DB: 15 Gaps: 0

US-10-817-483-2 (1-239) x ATU237588 (1-29524)

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QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40

Db 23015 CTTGCCAGACACTGGGCTTCCAGTCTTTCCTGATCGGCTCCAAATGTTCTCTCAG 23074
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
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Db 23135 CTGTAGATCGGCTCTGTGTGAAGGGTATCATCGCCAGCAAGCACTCATGAAGGCTG 23194
QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyLeuIleLeuGluGlyGlySerIle 100
Db 23195 ATGGGGAGAGTGTATATTATGAGGCCACGCGGCGCTTATTTCTGAGGAGGATCTATC 23254
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QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
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Db 23435 GAGCCTCGGCTGAGGCCCATCTGAAAGAGATGATGATGATGATGATGATGATGATGATG 23494
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuAspAlaAspMetGluAsn 200
Db 23495 GGTAGCCAGAACCAAGTCAATCCGATATGCTATTGCTGACCTGACCCCAATATGGAGAT 23554
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
Db 23555 AAGTTGATTCATGGATCCCTCAGAGATATCTCATTCATCATGACGCGGACAGAGACGAAA 23614
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 23615 TTCCCTCGAGTTAACGACCGCTTACAGCGGATTCGAAAGTCAATTCGGAATG 23671
RESULT 13
AB025109 1997 bp DNA linear BCT 27-MAR-1999
LOCUS AB025109
DEFINITION Agrobacterium tumefaciens gene for isopentenyl transferase,
complete cds.
ACCESSION AB025109
VERSION AB025109.1 GI:4586309
KEYWORDS isopentenyl transferase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 1997)
AUTHORS Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawaoka,A. and
Moriwae,N.
TITLE Agrobacterium tumefaciens plasmid P022 isopentenyl transferase (ipt)
gene
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 1997)
AUTHORS Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawaoka,A. and
Moriwae,N.
TITLE Direct Submision
JOURNAL Submitted (18-MAR-1999) Takehide Kasahara, Nippon Paper Industries
Co. Ltd. R&D Div., Wood Bio-engineering Central Research Lab.,
5-2-1, Oji, Kita-Ku, Tokyo 114-0002, Japan
(E-mail:takekewj.biglobe.ne.jp, Tel:81-3-3911-5106 (ex.292),
Fax:81-3-3914-3350)
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ALIGNMENT Scores:
Pred. No.: 1,416-106 Length: 1997
Score: 1052.00 Matches: 202
Percent Similarity: 92.5% Conservative: 19
Best Local Similarity: 84.5% Mismatches: 18
Query Match: 85.5% Indels: 0
DB: 15 Gaps: 0

US-10-817-483-2 (1-239) x AB025109 (1-1997)

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Db 688 ATGATATCTGCGTCTAATTTTCGGTCCAACTTGACAGAAAGACGTGACCGCGTAGCT 747
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerIleuAspArgValGlnCysCysProGln 40
Db 748 CTGGCCACGACACGCGGCTTCCAGTCTTTCGTCGATCGGAGTCCAAATGTTGCTCTCAG 807
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db 808 CTGTCAACCGGAAGCGGACGACCAACGTAAGAACTGAAGAAGCAAGCCGTCTATAC 867
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
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QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyLysLeuIleLeuGluGlyGlySerIle 100
Db 928 ATGGGAGAGTGTATATTATGAGCCCAAGCGGCGCTTATCTTGAGGAGGATCTATC 987
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
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QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
Db 1288 AAGTTGATTCATGGATGCTCAGAGATATCTCATTCATGCAAGCCGCAAGAACAGAAA 1347
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Db 1348 TTCCCTCGAGTTAACGACCGCTTACAGCGGATTCGAAAGTCAATTCGGAATG 1404

RESULT 14
LOCUS PLAT1PTG 1382 bp DNA linear BCT 11-NOV-1991
DEFINITION Plasmid T1 (from A. tumefaciens Tm-4) ipt gene for cytokinin.
ACCESSION X17428
VERSION X17428.1 GI:45558
KEYWORDS cytokinin; ipt gene; T1 plasmid.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE Bonnard,G., Tindland,B., Paulus,F., Szegedi,E. and Otten,L.
TITLE Nucleotide sequence, evolutionary origin and biological role of a
rearranged cytokinin gene isolated from a wide host range biotype
III Agrobacterium strain
JOURNAL Mol. Gen. Genet. 216 (2-3), 428-438 (1989)
PUBMED 2546041
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Score: 1050.00 Matches: 202
Percent Similarity: 92.0% Conservative: 16
Best Local Similarity: 85.2% Mismatches: 19
Query Match: 85.4% Indels: 0
DB: 15 Gaps: 0
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QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysGlyProGln 40
DB 272 CTTCGCCAGCAGACTGGGCTTCACATCTTCCTTCGCTCGATCGGATCCAAATGCTGTCCTAG 331
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuThr 60
DB 332 CTGTCAACCGGAGAGCGGACGACCAAGTGAAGACTGAAGAGAACCCCGCTGTGAC 391
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaIleGluArgLeu 80
DB 392 CTTGATGATCGGCCCTGCTGTGAAGGGTATCATCGACGACGAAAGCTCATGAGAGGCTG 451

QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyLeuIleLeuGluGlySerIle 100
DB 452 ATCCGGAGGGGTGAATTAATTATGAGCCGACCGGACTTATCTTGAGGGAGATCTATC 511
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 512 TCGTTGCTCAAGTCAATGCGCCAAAGCGGTATATGACCGCCGATTTTCGTTGCATATT 571
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
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DB 812 AAGTTGATTCATGGAGATCGCTCAGAGATATCTCATTCATGCGCGCTGGCAGAAACACGA 871
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPhe 237
DB 872 TTCCCGCCGTTGAGCCGCGCGCATCTTGAAGATTTGAAGCCACCATTC 922
RESULT 15
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LOCUS 10200 bp DNA linear BCT 18-APR-2005
DEFINITION A. tumefaciens Tm4 T1 plasmid DNA with TA-iaaH interrupted by 18866,
TA-iaaM, T-1pt and T-6 genes.
ACCESSION X56185
VERSION X56185.1 GI:39133
KEYWORDS iaaH gene; iaaM gene; indoleacetamide hydrolase; ipt gene;
isopentenyl transferase; tryptophane monooxygenase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE Bonnard,G., Tindland,B., Paulus,F., Szegedi,E. and Otten,L.
TITLE Nucleotide sequence, evolutionary origin and biological role of a
rearranged cytokinin gene isolated from a wide host range biotype
III Agrobacterium strain
JOURNAL Mol. Gen. Genet. 216 (2-3), 428-438 (1989)
PUBMED 2546041
REFERENCE Bonnard,G., Vincent,F. and Otten,L.
TITLE Sequence of Agrobacterium tumefaciens biotype III auxin genes
JOURNAL Plant Mol. Biol. 16 (4), 733-738 (1991)
PUBMED 1868204
REFERENCE Bonnard,G.
TITLE Direct Submision
AUTHORS Submitted (03-DEC-1990) G. Bonnard, INSTITUT DE BIOLOGIE
MOLECULAIRE DES, PLANTES DU CNRS, 12 RUE DU GENERAL ZIMMER, 67084
STRASBOURG CEDEX, FRANCE
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ORIGIN

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Alignment Scores:
Pred. No.: 2,35e-105 Length: 10200
Score: 1050.00 Matches: 202
Percent Similarity: 92.04 Conservative: 16
Best Local Similarity: 85.24 Mismatches: 19
Query Match: 85.44 Indels: 0
DB: 15 Gaps: 0
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US-10-817-483-2 (1-239) x ATTAIAAH (1-10200)

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QY      1 MetAapLeuAaYgLeuIleAaPheGlyProThrCySerThrglyVlySerThraIleAa 20
Db      7613 ATGATTCGCGCTTAAATTTTCGGTCCACTGACAGAAAGACGTCGACGGCATAGCT 7672

QY      21 LeuAaGlnGlnThrglyLeuProValLeuSerLeuAaPArGValGlnCySerProGln 40
Db      7673 CTGGCCACGACAGACTGGGCTTCAGCTCTTTTCGCTCGATCGGCTCAGTCTGCTCAG 7732

QY      41 LeuSerThrglySerGlyAaYgProThraValGlnLeuAaYgGlyThraThraGlyLeuYr 60
Db      7733 CTGTCAACCGAAGGAGGACGACCAACAGTGAAGAACTGAAGAAACACCCGCTCTGTAAC 7792

QY      61 LeuAaPArAaYgProLeuVallyGlyIleIleThraIlyGlnAaIleGlnAaYgLeu 80
Db      7793 CTTGATGATCGGCCCCCTGTGAAGGGVATCATCGGACCGGCAAGCTCATAGAGGCTG 7852

QY      81 IleAaGlnValIleAaSnIleGlnAaIlyGlyLeuIleLeuGlnGlyGlySerIle 100
Db      7853 ATCCGGGAGGCTGTATTAATTATAGAGCCACGCGGACCTTATTTGAGAGGAGACTATTC 7912

QY      101 SerLeuLeuAaYgCySerMetIleGlnSerAaYgTyrTrpAaAaIleAaPheAaYgTrpHisIle 120
Db      7913 TCGTTGCTCAAGTGCATGCGCCAAAGCCGTTATTGAGCGCCGATTTTCGTTGCGCATATT 7972

QY      121 IleAaGlnGlnLeuAaIleAaGlnGlnLeuSerPheMetSerValAaIlySerThraYVallys 140
Db      7973 ATTCGCCACCAAGTTAGACGAGGAGGACCTTCATGAAGAGCGCCAGAGCTTAAAG 8032

QY      141 GlnMetLeuAaYgProSerAaIleGlyLeuSerIleIleGlnGlnLeuValGlnLeuYrPArG 160
Db      8033 CAGATGTTGTGCCCCCGCTATAGGCCCATCTCTATTCAAGAGTTGGTTATCTTTGCAAT 8092

QY      161 GluProAaYgLeuAaYgProIleLeuGlnGlyIleAaPgiYrAaYgYrAaIleuLeuPhe 180
Db      8093 GAGCCTCGGCTGAGGCGCCATACCTGAAGAGATCATGATGATATCATGATGCTGTTT 8152

QY      181 AlaThrglnAaGlnIleThraProAaPheMetLeuGlnLeuAaPArAaIleAaPheGln 200
Db      8153 GCTACCCAGAAATCGGATACCCCGCATVGTGATTATTCAGCTTGAGCGAGATATGAGAGGT 8212

QY      201 LysLeuIleIleGlyIleAaGlnGlnPheLeuIleIleAaAaYgAaYgGlnGlnIlyns 220
Db      8213 AAGTTGATTCATGGATGCTCAGAGAGATCTCATTCATGCGCGGACAGAACACAGAA 8272

QY      221 PheProLeuValGlyAaIleThraIleValGlnAaPheGlnGlyProProPhe 237
Db      8273 TTCCGCGCGGTGAGGCGGCGAGCTTTGAAAGATTGAAGGCCACCATTC 8323
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Search completed: June 26, 2006, 21:30:23

Job time : 5814 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 19:29:08 ; Search time 652 Seconds

(without alignments)
3833.667 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
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Listing first 45 summaries

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1230	100.0	717	13	ADS63261 Bacterial
2	1230	100.0	721	3	AAc86514 Nucleotide
3	1230	100.0	723	10	ACF58155 Z. mays 1

4	1230	100.0	1919	13	ADT92127 A. tumefaciens
5	1230	100.0	2722	3	AAc86508 DNA const
6	1230	100.0	2722	3	AAc86507 DNA const
7	1230	100.0	3017	3	AAc86511 DNA const
8	1230	100.0	5622	3	AAc86506 DNA const
9	1075	87.4	720	13	ADS63280 Bacterial
10	1075	87.4	720	13	ADS63264 Bacterial
11	1075	87.4	720	13	ADS59368 Bacterial
12	1075	87.4	720	13	ADS62875 Bacterial
13	1075	87.4	723	13	ADT62691 DNA encod
14	1068	86.8	723	13	ADRA42934 IPT-like
15	1068	86.8	723	13	ADRA42936 IPT-like
16	1068	86.8	723	15	AEFI1453 Isopenten
17	1068	86.8	723	15	AEFI1472 Isopenten
18	1066	86.7	720	13	ADS63295 Bacterial
19	1052	85.5	720	13	ADS63294 Bacterial
20	1052	85.5	1997	12	ADOS5756 Agrobacte
21	1050	85.4	720	13	ADS63275 Bacterial
22	1050	85.4	720	13	ADS63279 Bacterial
23	1050	85.4	723	13	ADRA42938 IPT-like
24	1050	85.4	723	13	ADRA42940 IPT-like
25	1050	85.4	723	15	AEFI1470 Isopenten
26	1050	85.4	723	15	AEFI1468 Isopenten
27	1035	84.1	777	13	ADS63297 Bacterial
28	1005	81.7	720	13	ADS63266 Bacterial
29	1005	81.7	720	13	ADS63290 Bacterial
30	1005	81.7	720	13	ADS63262 Bacterial
31	1005	81.7	720	13	ADS63292 Bacterial
32	1005	81.7	723	3	AAAD0619 Agrobacte
33	1005	81.7	745	2	AAV69757 Isopenten
34	1005	81.7	1388	6	ABK12492 Agrobacte
35	1005	81.7	2595	11	ADJ99856 IPT gene
36	1005	81.7	2595	11	ADL73033 Agrobacte
37	1005	81.7	2595	14	ADX69862 Isopenten
38	1005	81.7	9323	10	ADJ99857 Binary ve
39	1005	81.7	9323	14	ADX69863 Plasmid p
40	1005	81.7	24596	1	AAV50182 Complete
41	995	80.9	3182	6	AAV50182 A. thaliana
42	995	80.9	24593	1	AAV50226 Sequence
43	994	80.8	747	3	AAV50624 Agrobacte
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ALIGNMENTS

RESULT 1
ADS63261
ID ADS63261 standard; cDNA; 717 BP.
XX
XX ADS63261;
AC
AC
DT 02-DEC-2004 (first entry)
XX
XX Bacterial polynucleotide #15248.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
XX Bacteria.
OS
PN US2003233675-A1.
XX
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR

XX (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 38935; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 717 BP; 180 A; 176 C; 190 G; 171 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,16e-132 Length: 717
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0
US-10-817-483-2 (1-239) x ADS63261 (1-717)
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DB 1 ATGATCTACGCTTAATTTTGGGTCCAACTTGCAAGAGAAAGACATCAGCTGCACTACT 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTGGCCAGCAGACAGCGCTCCCACTCTCTCGCTCGATCCGCTCAATGCTGCTCTCA 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuLys 60
DB 121 CTATCAACCGGAAGGGGCGACCAACAGTGAAGAACTGAAGGAACACCTCGTCTGTAC 180
QY 61 LeuAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
DB 181 CTGATGATCGCCCTTTGGTAAAGGTATCATTAAGCCAAAGCAAGCTCATGAACGGCTC 240
QY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyLeuIleLeuGluGlyCysIle 100
DB 241 ATTGGGAGGTGACCAATCACAGAGCCAAAGGGGGCTTAATCTTGAAGGAGATCTATC 300

QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAGTGCATGAGCGCAAGTGTATTGAAACGGGAAATTTTCGTTGGCATATT 360
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 361 ATTGCAAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCGTGGCCAAAGACCAAGATTAA 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACCCCTCTGCAAGGTCTTCTATTATTCAAAGATTGTTCACTTTGAGG 480
QY 161 GluProArgLeuAspProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCCTCGGCTGAGGCCCATCTGAAAGGATCATGATTCATATGCTCCCTGCTATT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTACCCAGAACGATCAGCCCGATATGCTATTGAGCTCGACGCGATATGAGAAAT 600
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
DB 601 AAATTGATTCAAGGTATCGCTCAGAGATTCTTAATCCATGCGCGCTCGACAGAAACAGAA 660
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 661 TTCCTTTGGTGGGCGGACAGCTGTGAAACGTTTGAAAGCACCATTTTCGAATG 717
RESULT 2
AAC86514
ID AAC86514 standard; DNA; 721 BP.
XX
AC AAC86514;
XX
DT 19-MAR-2001 (first entry)
XX
DE Nucleotide sequence of an isopentenyl transferase (ipt) gene fragment.
XX
KW temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KW ipt; ss.
XX
OS Agrobacterium tumefaciens.
XX
PN WO20063401-A1.
XX
PD 26-OCT-2000.
XX
PE 13-APR-2000; 2000WO-US009943.
XX
PR 16-APR-1999; 99US-0129844P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Habben JE, Zinselmeier C, Tomes D;
XX
DR WPI; 2000-672743/65.
XX
PT Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 16; 76pp; English.
XX
CC The present sequence represents an isopentenyl transferase gene fragment.
CC The fragment was used to produce the recombinant DNA molecules of the
CC invention. These comprise a genetic construct consisting of a promoter
CC directing temporal and/or spatial gene expression in plant seed
CC operatively linked to a cytokinin modulating gene. The recombinant DNA
CC molecules are useful for producing fertile, transgenic plants capable of
CC regulated expression of a cytokinin modulating gene in developing seeds.

CC They are also useful for improving stress tolerance and yield stability
CC in plants. The preferential expression of recombinant DNA molecules of
CC the invention occurs about 14-25 days after pollination. The transgenic
CC plants thus produced have enhanced levels of cytokinin expression exhibit
CC improved seed size, decreased tip kernel abortion and increased seed set
CC during unfavourable environmental conditions

XX Sequence 721 BP, 182 A, 176 C, 191 G, 172 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	1,16e-132	Length:	721
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-817-483-2 (1-239) x AAC6514 (1-721)

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OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysProGln 40
DB 62 CTGGCCGACGACAGCTGGCTCCCAAGTCTCTCGTCGATCGGTCCTCAATGCTCTCA 121
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 122 CTATCAACCGGAAGGGGCGACCAACATGGGAAGACTGAAGAACACATCGTCTGAC 181
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 182 CTGATGATCGCCCTTTGGTAAAGGATATCATTAACGACCAAGCATCATGAACGGCTC 241
OY 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLysGlyLeuGluGluGlySerIle 100
DB 242 ATGGGAGGAGTGCACAATCACAGAGCCAAAGCGGCTTATCTTGAGGAGATCTATC 301
OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTPAsnAlaAspPheArgTrpHisIle 120
DB 302 TCGTTCCTCAGGTGCATGGCGCAAGTCTTATTGGAACGGGATTTTCGTTGGCATATT 361
OY 121 IleArgAsnGluLeuAlaAspGluLysPheMetSerValAlaLysThrArgValLys 140
DB 362 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGGTGCCAAGCCAGATTAAG 421
OY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 422 CAGATGTTACGCCCTCTGCAAGTCTTCTATTATCCAAAGTGTGTTCAACTTTGGAGG 481
OY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 482 GAGCTCGGCTGAGGCGCCATCTGGAAGGATCGATGGATATCGATATGCTCTATTT 541
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 542 GCTACCCAGAACCAATCATCGCCGATATGCTATTGCAAGCTCGACGACGATATGAGAT 601
OY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
DB 602 AAATTGATTCACGGGTATCGCTCAGAGTTTCTAATCCATGCGCGTCGACAGGAACAGAA 661
OY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 662 TTCCTTTGGTGGGCGACAGCTGTCAAGGCTTTGAAGACCACTTTGCAATG 718
```

RESULT 3

ACF58155
ID ACF58155 standard; cDNA; 723 BP.
XX ACF58155;
XX

DT 15-JAN-2004 (first entry)

XX Z. mays isopentenyl transferase encoding cDNA.

DE Z. mays isopentenyl transferase; transformation; transgenic; gl2; cell division;

KW isopentenyl transferase; gene; ss.

XX Zea mays.

XX Key Location/Qualifiers

FT CDS 1..723

FT /tag= a

FT /product= "isopentenyl transferase"

XX WO2003087313-A2.

XX 23-OCT-2003.

XX 08-APR-2003; 2003WO-US010544.

XX 08-APR-2002; 2002US-0370796P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Zinselmeier C, Helentjaris TG;

XX WPI; 2003-845315/78.

DR P-PSDB; ABR61587.

PT Enhancing silk exsertion in a Zea mays plant under stress, relative to a

PT non-transformed Zea mays plant under stress by transforming the plant or

PT its ancestor with a construct comprising a silk-specific or silk-

PT preferred promoter.

PS Claim 2; Page 67-68; opp; English.

CC The invention relates to enhancing silk exsertion in a Zea mays plant

CC under stress, relative to a non-transformed Zea mays plant under stress.

CC The method involves transforming the plant or its ancestor with a

CC construct comprising a silk-specific or silk-preferred promoter operably

CC linked to a polynucleotide encoding a polypeptide that increases cell

CC division. The present sequence represents a cDNA encoding a Z. mays

CC isopentenyl transferase, a polypeptide involved in cell division

XX Sequence 723 BP, 181 A, 176 C, 192 G, 174 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	1.17e-132	Length:	723
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-817-483-2 (1-239) x ACF58155 (1-723)

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OY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGATCTACGCTCAATTTTCGGTCCAACTTCACAGGAAGACATCGACTCGATAGCT 60
OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysProGln 40
DB 61 CTGGCCGACGACAGCTGGCTCCCAAGTCTCTCGTCGATCGGTCCTCAATGCTCTCA 120
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 121 CTATCAACCGGAAGGGGCGACCAACATGGGAAGACTGAAGGAAGACATCGCTGTAC 180
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 181 CTGATGATCGCCCTTTGGTAAAGGATATCATTAACGCAAGCATGAACGGCTC 240
OY 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLysGlyLeuGluGluGlySerIle 100
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Db 241 ATTGGAGAGGTGACAAATCACAGAGCCCAAAGCGGGCTTATTCTTGAGGAGATCTATTC 300
Qy 101 SerleuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGGCTCAGAGTGCATGGCCAAAGTCGTTATTGGAACGGGAGATTTTCGTTGGCATATTT 360
Qy 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaIleThrArgValIys 140
Db 361 ATTGGCAACGAGTTAGCAGACGAGAGAGGCTTCATGACCGTGCCCAACAGAGTTAAG 420
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 421 CAGATTGTTAGCCCTCTTCAGAGTCTTTCTATTATCCAAAGTTGCTTCACTTTGGAGG 480
Qy 161 GluProArgLeuArgProIleLeuGlnGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 481 GAGCTGGGCTGAGAGCCCATATCTGGAAGGATTCGATATTCGATATGCCCTGTATTT 540
Qy 181 AlathrglnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCCAAGAACCGATCACCCCGCATATGCTATTGACGCTCGACGAGATATGAGAAAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnIleLys 220
Db 601 AAATTGATTCCAGGATGCTCCTCAGAGTTTCTTAATCCATGCGCGCTCGACAGAACAGAAA 660
Qy 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCCTTTGGTGGGGCGACAGCTGTGCAAGGTTTGAAGACCACTTCGAATG 717

RESULT 4

ADT92127
ID ADT92127 standard; DNA; 1919 BP.

AC ADT92127;

DT 13-JAN-2005 (first entry)

DE A. tumefaciens isopentenyl transferase (ipt) encoding DNA.

KW ipt; transgenic; plant; cytokinin; female reproduction;
isopentenyl transferase; plant breeding; gene; ds.

OS Agrobacterium tumefaciens.

FH Key Location/Qualifiers
CDS 690..1409
/*tag= a
/product= "ipt"

XX MO2004090143-A2.

XX 21-OCT-2004.

XX 02-APR-2004; 2004WO-US010664.

XX 04-APR-2003; 2003US-0460718P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Haben JE, Zinselmeier C, Tomes DT, Abbitt SE, Helentjaris TG;
PI Niu X;

XX WPI; 2004-748771/73.

XX P-PSDB; ADT92128.

XX GENBANK; X14410.

XX Producing transgenic plants capable of regulated expression of cytokinin-
modulating gene comprises transformation of plant cells with a genetic
construct capable of temporally- or spatially-regulated expression of
cytokinin modulating gene.

BS Claim 37; SEQ ID NO 1; 157bp; English.

CC The invention relates to producing transgenic plants capable of the
CC regulated expression of a cytokinin-modulating gene in developing seed or
CC related female reproductive tissue. The method involves transformation of
CC plant host cells with a genetic construct capable of temporally- or
CC spatially-regulated expression of a cytokinin modulating gene in
CC developing seed or related female reproductive tissue, and regenerating
CC and recovering the transgenic plants. The transformation is carried out
CC by electroporation, PEG poration, particle bombardment, silicon fiber
CC delivery, microinjection, or Agrobacterium-mediated transformation. The
CC genetic construct comprises a promoter directing temporal or spatial gene
CC expression in developing seed or related female reproductive tissue,
CC operably linked to a cytokinin-modulating gene. The promoter is selected
CC from 2a2g2.1, zap, tbi, eep1, eep2, F3.7, ttxh, Zm40, ESR, PCNA2, lcc1,
CC ZmCkx1-2, ZmCkx2, ZmCkx4, or ZmCkx5. The cytokinin-modulating
CC gene is selected from genes encoding cytokinin biosynthetic enzymes,
CC cytokinin catabolic enzymes, cytokinin catabolic enzyme antagonists, or
CC cytokinin biosynthetic enzyme agonists. The method is useful for
CC producing transgenic plants having enhanced cytokinin activity.
CC Transgenic plants exhibit useful characteristics including improved seed
CC size, decreased tip kernel abortion, or stability of yield. The probes
CC that hybridize to cytokinin metabolic enzyme polynucleotide sequences are
CC useful as molecular markers in breeding programs. The inhibitors to the
CC polypeptides are useful for modulating the activity and/or expression of
CC the polypeptides. The products, compositions, processes, and methods
CC above are useful for research, biological, and agricultural purposes. The
CC present sequence represents a DNA encoding an A. tumefaciens isopentenyl
CC transferase (ipt) enzyme.

SQ Sequence 1919 BP; 533 A; 378 C; 441 G; 567 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.7e-132	Length:	1919
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	13	Gaps:	0

US-10-817-483-2 (1-239) x ADT92127 (1-1919)

Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysTrpSerThrAlaIleIle 20
Db 690 ATGATCTACGCTTAATTTTGGTCCAACTGCACAGAAAGAAATCAGCTGCAATGACT 749
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 750 CTGGCCACGACAGACTGGCTCCAGTCTCTCGCTCATGCCGTCCTCAATGCTGCTCA 809
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
Db 810 CTATCAACCGGAAACGGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAAC 869
Qy 61 LeuAspAspArgProLeuValIleGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
Db 870 CTGATGATCGCCCTTTGGTAAAGGATATCTTACAGCAAGCAAGCTCAAGACGGCTC 929
Qy 81 IleAlaGluValHisAsnHisGlnAlaLysGlyLeuIleLeuGlnGlyGlySerIle 100
Db 930 ATTGGAGAGTGCACATACAGAGCCCAAGCGGGCTTATCTTGAGGAGATCTATTC 989
Qy 101 SerleuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 990 TCGTTGGCTCAGAGTGCATGGCCAAAGTCGTTATTGGAACGGGAGATTTTCGTTGGCATATTT 1049
Qy 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaIleThrArgValIys 140
Db 1050 ATTGGCAACGAGTTAGCAGACGAGAGGCTTCATGACCGTGCCCAACAGAGTTAAG 1109
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160

DB 1110 CAGATGTTACGCCCTCTGACGCTCTTTCTATTATCCAAAGATTGGTTCAACTTTGGAGG 1169
QY 161 GIUProArGLeuArGProIleLeuGluGlyIleAspGlyTYrArgTYrAlaLeuPhe 180
DB 1170 GAGCTCGGCTGAGGCCCATCTAGTGAAGGATCGATGATATGATATGCCCTGCTATTT 1229
QY 181 AlAThrgInaAngInIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 1230 GCTACCCAGAACCAATGATCAGCCCGCATATGCTATTGTCAGCTCGACGATATGAGAAAT 1289
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGln 220
DB 1290 AAATTGATTCAAGGATGCTAGAGATTCTTAATCTCATGCGCGTCAAGACAGAAACAGAA 1349
QY 221 PheProLeuValGlyAlaThraIaValaGluAlaPheGluGlyProProPheArgMet 239
DB 1350 TTCCTTTGGTGGGGCGGACAGCTGTCCAGAGCTTTGAAGACCAACCATTTGGAATG 1406
RESULT 5
AAC86508 1D AAC86508 standard; DNA; 2722 BP.
AC AAC86508;
AC AAC86508;
DT 19-MAR-2001 (first entry)
XX
DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
XX
KW temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
XX
XX Synthetic.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Solanum tuberosum.
XX WO200063401-A1.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000MO-US009943.
XX
PR 16-APR-1999; 99US-0129844P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Habben JE, Zinselmeier C, Tomes D;
XX
XX WPI; 2000-672743/65.
DR
XX
PT Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 70-71; 76pp; English.
XX
CC The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a maize promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a Solanum
CC tuberosum terminator. The DNA molecules of the invention comprise a
CC genetic construct consisting of a promoter directing temporal and/or
CC spatial gene expression in plant seed operatively linked to a cytokinin
CC modulating gene. The recombinant DNA molecules are useful for producing
CC fertile, transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving
CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions

XX
SQ Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7,73e-132 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-817-483-2 (1-239) x AAC86508 (1-2722)
QY 1 MetaAspLeuArGLeuIlePheGlyProThrCysThrglyYrThSerThraIleAla 20
DB 1525 ATGATCTACGCTATATTTCCGTCACATTCGACAGAAAGACATCGACTCGATAGCT 1584
QY 21 LeuAlaGlnGlnThnglyLeuProValLeuSerLeuAspArgValGlnCysGlyProGln 40
DB 1585 CTTCGCCAGACAGACTGGCTCCCAAGTCTCTCGCTCGATCGGTCCAATGCTCTCA 1644
QY 41 LeuSerThrglySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTYr 60
DB 1645 CTATACACCGAAGCGGGCGACCAACAGTGAAGAACTGMAAGAACAGACTGCTGTAC 1704
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThraIaLysGlnAlaHisGluArgLeu 80
DB 1705 CTGATGATCGCCCTTTGGTAAAGGATATTCATACGACCAAGCATCATACGCGCTC 1764
QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyLeuIleLeuGlnGlyGlySerIle 100
DB 1765 ATTCGGAGGAGGACCAATCACAGAGCCCAAGCGGGCTTATCTTGAAGGAGATCTATC 1824
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTYrTPAsnAlaAspPheArgTYrHisIle 120
DB 1825 TCGTTGCTCAAGTGCATGCGGCAAGTCTTATTTGAACCGCGATTTTCGTTGGCATATT 1884
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 1885 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCTGCGCAACAGACTTAAAG 1944
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTYrArg 160
DB 1945 CAGATGTTACGCCCTCTGACAGGCTCTTCTATTAACCAAGATTGGTTCAACTTTGGAGG 2004
QY 161 GIUProArGLeuArGProIleLeuGluGlyIleAspGlyTYrArgTYrAlaLeuPhe 180
DB 2005 GAGCTCGGCTGAGGCCCATCTAGTGAAGGATCGATGATATGATATGCCCTGCTATTT 2064
QY 181 AlAThrgInaAngInIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 2065 GCTACCCAGAACCAATGATCAGCCCGCATATGCTATTGTCAGCTCGACGATATGAGAAAT 2124
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGln 220
DB 2125 AAATTGATTCAAGGATGCTCAGAGATTCTTAATCCATGCGCGTCAAGAACAGAA 2184
QY 221 PheProLeuValGlyAlaThraIaValaGluAlaPheGluGlyProProPheArgMet 239
DB 2185 TTCCTTTGGTGGGGCGGACAGCTGTCCAGAGCTTTGAAGACCAACCATTTGGAATG 2241
RESULT 6
AAC86507 1D AAC86507 standard; DNA; 2722 BP.
AC AAC86507;
AC AAC86507;
DT 19-MAR-2001 (first entry)
XX
DE DNA comprising a barley promoter and Agrobacterium ipt gene.
XX
KW temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;

KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KM ipt; ss.
XX
XX Synthetic.
OS Hordeum vulgare.
OS Agrobacterium tumefaciens.
OS Zea mays.
XX
XX WO20063401-A1.
XX
XX 26-OCT-2000.
XX
XX 13-APR-2000; 2000WO-US009943.
XX
XX 16-APR-1999; 99US-0129844P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Haben JE, Zinselmeier C, Tomes D;
XX
XX WPI; 2000-672743/65.
XX
XX Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
XX
XX Disclosure; Page 69-70; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a barley promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
CC terminator. The DNA molecules of the invention comprise a genetic
CC construct consisting of a promoter directing temporal and/or spatial gene
CC expression in plant seed operatively linked to a cytokinin modulating
CC gene. The recombinant DNA molecules are useful for producing fertile,
CC transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving
CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions
XX
XX Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 7,73e-132 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-817-483-2 (1-239) x AAC86507 (1-2722)

QY 1 MetAspLeuAArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleA 20
DB 1525 ATGATCTACGTCCTAATTTCGTCCTCAACTGACAGAAAGACATCGACTGCGATACT 1584
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 1585 CTTCGCCAGCAGACTGGCTCCCAAGTCCCTGCTCGATCGGTCGAATGCTGCTCA 1644
QY 41 LeuSerThrGlySerGlyAArgProThrValGlnGluLeuLysGlyThrThraGluLeu 60
DB 1645 CTATTAACCGGAAGCGGCGACCAACAGTGGAGAAGACTGAAGAACACTGCTGTAC 1704
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThraLysGlnAlaHisGlnArgLeu 80
DB 1705 CTTGATGATCGCCCTTTGGTAAAGGGTATCATTAACGCAAGCATCATGAACGGCTC 1764
QY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyGlyLeuIleLeuGlnGlyGlySerIle 100

DB 1765 ATTCGGAGGGTGCACATTCACAGAGCCCAAGCGGCTTATTCTTAGAGGAGATCTATC 1824
QY 101 SerLeuLeuArgCysMetAlaGlnSerAArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 1825 TCGTTGGCTCAGAGTGCATAGCGGCACAAAGTCGTATTGGAACCGGATTTTCGTTGGCATAT 1884
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 1885 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGCGCCAGACAGAGTTAAAG 1944
QY 141 GlnMetLeuAArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 1945 CAGATGTTACGCCCTCTGCAGGTCCTTCTATTATCCAAAGAGTTGTTCACTTTGAGAG 2004
QY 161 GluProArgLeuAArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 2005 GAGCCTGGGCTGAGGCCCATCTGGAAGGATCGATGATATGCTATGCTGCTATTT 2064
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 2065 GCTACCCAGAACCAAGATCACGCCCGATATGCTATTGACGCTCGACGACGATATGAGAT 2124
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaAArgGlnGluGlnLys 220
DB 2125 AAATTGATTCCAGGTTATGCTCAGAGATTCTAATCCATGCGCGCTCCACAGGAACAGAA 2184
QY 221 PheProLeuValGlyAlaThrAlaValAlaGlnLeuGluGlyProProPheArgMet 239
DB 2185 TTCCCTTGTGGGCGGACAGCTGCGAAGCGTTTGAAAGAGCACCATTTGCAATG 2241

RESULT 7
AAC86511
ID AAC86511 standard; DNA; 3017 BP.
AC AAC86511;
AC 19-MAR-2001 (first entry)
DT 19-MAR-2001 (first entry)
XX
XX DNA construct comprising a maize promoter and Agrobacterium ipt gene.
DE
XX
XX temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KM ipt; ss.
XX
XX
XX Synthetic.
OS Zea mays.
OS Agrobacterium tumefaciens.
XX
XX WO20063401-A1.
XX
XX 26-OCT-2000.
XX
XX 13-APR-2000; 2000WO-US009943.
XX
XX 16-APR-1999; 99US-0129844P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Haben JE, Zinselmeier C, Tomes D;
XX
XX WPI; 2000-672743/65.
XX
XX Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
XX Disclosure; Page 72-73; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a maize promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize

CC terminator. The DNA molecules of the invention comprise a genetic
 CC construct consisting of a promoter directing temporal and/or spatial gene
 CC expression in plant seed operatively linked to a cytokinin modulating
 CC gene. The recombinant DNA molecules are useful for producing fertile,
 CC transgenic plants capable of regulated expression of a cytokinin
 CC modulating gene in developing seeds. They are also useful for improving
 CC stress tolerance and yield stability in plants. The preferential
 CC expression of recombinant DNA molecules of the invention occurs about 14-
 CC 25 days after pollination. The transgenic plants thus produced have
 CC enhanced levels of cytokinin expression exhibit improved seed size,
 CC decreased tip kernel abortion and increased seed set during unfavourable
 CC environmental conditions

XX
 SQ Sequence 3017 BP; 865 A; 679 C; 622 G; 851 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8_95e-132	Length:	3017
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-817-483-2 (1-239) X AAC86511 (1-3017)

```

QY      1 MetAapleuAArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleA 20
DB      1408 ATGGATCTACGCTAATTTTCGGTCCACCTTGACAGAAAGCATCGACTGGATAGCT 1467
QY      21 LeuAlaGlnGlnThGlyLeuProValLeuSerLeuAparValGlnCysCysProGln 40
DB      1468 CTTGCCACAGACTGGCTCCAGTCTCTGCTGCTGATGCGCTCAATGCTGTCTCA 1527
QY      41 LeuSerThGlySerGlyAArgProThrValGlnGlnLeuLysGlyThrThraArgLeuYr 60
DB      1528 CTATCAACCGGAAGGGGGGCGACCAACAGTGAAGAACTGAAGAAAGCATGCTGCTGAC 1587
QY      61 LeuAapAparAArgProLeuValLysGlyIleIleThraIleLysGlnAlaHisGlnArgLeu 80
DB      1588 CTTGATGATGCGCTTTGGTAAAGGATATCATTTACGCCACAGCAAGCTCATGACCGCTC 1647
QY      81 IleAlaGlnValHisAsnHisGlnAlaLysGlyIleuIleLysGlnGlySerIle 100
DB      1648 ATTGGGAGGTGCACATACAGAGGCGGAGGCTTATCTTGAGGAGGATCTATC 1707
QY      101 SerLeuLeuAArgCysMetAlaGlnSerAArgYTrpAsnAlaAparPheArgTrpHisIle 120
DB      1708 TCGTTGCTCAGGTGATGCGCGCAAGTCTTATTTGAAACGCCGATTTTCTTGCGCATATT 1767
QY      121 IleArgAargGlnLeuAlaAparGlnGlnSerPheMetSerValAlaLysThraArgValLys 140
DB      1768 ATTTCCCAACGAGTGTGACACAGAGGAGCTTCATGAGCGTGCACCAAGACAGAGTTAAG 1827
QY      141 GlnMetLeuAArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
DB      1828 CAGATGTTAGCCCTCTGCAAGTCTTCTTATTTATCCAAAGTGGTTCAACTTTGGAAG 1887
QY      161 GlnProAArgLeuAArgProIleLeuGlnGlyIleAparGlyTyrArgGlyAlaLeuPhe 180
DB      1888 GAGCCTCGGCTAGAGCCCATATCTGGAAGGATCGATGATATCGATATCCCTGCTATTT 1947
QY      181 AlaThrGlnAargGlnIleThrProAparMetLeuLeuGlnLeuAparAlaAparMetGlnA 200
DB      1948 GCTACCCAGAACACAGATCACGCCCGATATGCTATTTGACCTCGACCCACATATGGAAT 2007
QY      201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaAArgGlnGlnGlnLys 220
DB      2008 AATATGATTCACGGATTCCTCAAGAGTTCTTAATCCATGCGCTGACAGAAACGAA 2067
QY      221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB      2068 TTCCTTTGTTGGTGGGGGCGACACGCTGCGAAGCGTTTGAAGAGCACCATTTTGANTG 2124
  
```

RESULT 8

AAC86506
 ID AAC86506 standard; DNA; 5622 BP.

XX AAC86506;

XX 19-MAR-2001 (first entry)

DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.

XX temporal gene expression; spatial gene expression; plant seed;

KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;

KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;

XX ipt; ss.

XX Synthetic.

OS Zea mays.

OS Agrobacterium tumefaciens.

XX WO200063401-A1.

XX 26-OCT-2000.

XX 13-APR-2000; 2000WO-US009943.

XX 16-APR-1999; 99US-0129844P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Haben JE, Zinselmeier C, Tones D;

XX WPI; 2000-672743/65.

XX Novel recombinant DNA construct useful for producing transgenic plants

PT having enhanced levels of cytokinin expression, improved stress tolerance

PT and yield stability.

XX Disclosure; Page 67-69; 76pp; English.

XX The present sequence represents a recombinant DNA molecule of the

CC invention. It comprises, in this order, a maize promoter, an

CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize

CC terminator. The DNA molecules of the invention comprise a genetic

CC construct consisting of a promoter directing temporal and/or spatial gene

CC expression in plant seed operatively linked to a cytokinin modulating

CC gene. The recombinant DNA molecules are useful for producing fertile,

CC transgenic plants capable of regulated expression of a cytokinin

CC modulating gene in developing seeds. They are also useful for improving

CC stress tolerance and yield stability in plants. The preferential

CC expression of recombinant DNA molecules of the invention occurs about 14-

CC 25 days after pollination. The transgenic plants thus produced have

CC enhanced levels of cytokinin expression exhibit improved seed size,

CC decreased tip kernel abortion and increased seed set during unfavourable

CC environmental conditions

SQ Sequence 5622 BP; 1546 A; 1295 C; 1189 G; 1592 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2_17e-131	Length:	5622
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-817-483-2 (1-239) X AAC86506 (1-5622)

```

QY      1 MetAapleuAArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleA 20
DB      1525 ATGGATCTACGCTAATTTTCGGTCCACCTTGACAGAAAGCATCGACTGCGATAGCT 1584
QY      21 LeuAlaGlnGlnThGlyLeuProValLeuSerLeuAparValGlnCysCysProGln 40
  
```

Db 1585 CTTGCCACGACGAGCTGGCCCTCCAGTCTCTCGCTCCATCGCGTCCATGCTGTCTCA 1644
Qy 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db 1645 CTTATCAACCGGACCGGGCGACCAACAGTGAAGAACTGAAGAACGACCTGCTGTAC 1704
Qy 61 LeuAspAspArgProLeuValLysGlyYlleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 1705 CTTATGATGCGCCCTTGTGTAAAGGATATTCATTCAGCCAAAGCAAGCTCATGAACGGCTC 1764
Qy 81 IleAlaGluValHisAsnHisGluAlaLysGlyLysLeuLysGluGlyGlySerIle 100
Db 1765 ATTGGGAGGTCGCAACATCAAGAGCCAAAGCGGGCTATTCTTTGAGGAGATCTATC 1824
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTyrHisIle 120
Db 1825 TCGTTGCTCAGAGTCATGCGCCAAAGTCGTATTGGAACGCGGATTTTCGTTGCGATATT 1884
Qy 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db 1885 ATTGCAACGAGTTAGACAGACGAGAGAGCTTCATGACCGTGGCCAGACCAAGATTAAG 1944
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTyrArg 160
Db 1945 CAGATGTTACGCCCTCTGACAGGCTTTCTATTATCCAAAGTTGGTTCACTTTGAGAG 2004
Qy 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 2005 GAGCTCGGCTGAGAGCCCATCTGTAAGAGATCGATGATTCGATATGCCCTCTATTAT 2064
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAlaAspMetGluAsn 200
Db 2065 GCTATCCCAAGAACCGATACCGCCGATATGCTATTGACGCTCGAGCAGATATGAGAT 2124
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
Db 2125 AAATTGATTCACGGATATGCTCAGAGATTCTTAATCCATGCGCGCTCGACAGAAACAGAA 2184
Qy 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 2185 TTCCCTTGTGTGGCGGACAGCTGTGAAACGTTTGAAGACCACTTCATTCGATG 2241
RESULT 9
ADS63280
ID ADS63280 standard; cDNA, 720 BP.
XX
AC ADS63280;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #15267.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
FR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 38954; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 720 BP; 182 A; 166 C; 197 G; 175 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,11e-114 Length: 720
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: Gaps: 13
US-10-817-483-2 (1-239) X ADS63280 (1-720)
Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db 1 ATGATATCGCTCTTAATTTTCGTGCCAATTCGACAGAAAGAGCTGACCGCGTAGCT 60
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 61 CTTCCCAAGCAAGATCGGCTTCAGTCCTTTCCCTCGATCGGGTCCAAATGTTGCTCTCAG 120
Qy 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyYlleIleThrArgLeuTyr 60
Db 121 CTTGTCACCGGACCGGACGACCAACAGTGAAGAACTGAAGAAAGAGCGCTTATAC 180
Qy 61 LeuAspAspArgProLeuValLysGlyYlleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 181 CTTATGATGCGCCCTTGTGTAAAGGATATTCATTCAGCCAAAGCAAGCTCATGAAGGCTG 240
Qy 81 IleAlaGluValHisAsnHisGluAlaLysGlyLysLeuLysGluGlyGlySerIle 100
Db 241 ATGGGAGAGGTGTATTATATGAGGCCCAAGCGGGCTATTCTTTGAGGAGATCTATC 300
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTyrHisIle 120
Db 301 TCGTTGCTCAAGTCATGCGCCAAAGCTTATTGAGATGCGGATTTTCGTTGCGATATT 360

QY 121 IleaTgaSngLleuAlaSpGluSerPheMetSerValAlaIleThrArgVallys 140
DB 361 ATTCGCCAGAGTTGACGAGACGAAAGACCTTCATGAACTGGCCAAAGCCAGATTAAAG 420
QY 141 GlnMetLeuArgProSerIleAglyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTGCTGCAGAGCCCTTCTATTATTCAGAACTGGTTGATCTTTGGAAA 480
QY 161 GlnProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCTTCGGCTGACGCCCCACTACTGAAAGATCGATGATATCGATATCCATGTTGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTACCCAGAACCAAGTCCATCCGATATGTCATTGACAGCTTGACGACATATGAGAGAT 600
QY 201 LysLeuIleIleGlyIleAlaGlnGluPheLeuIleIleAlaArgArgGlnGluGln 220
DB 601 AAGTTGATTTCATGGAGTCCCTCAGAGTATCTCATTCATGACGCGCAGACAGAACGAAA 660
QY 221 PheProLeuValGlyValaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 661 TTCCCTCAGATTACGACGAGCCGCTTACGACGATTGCAAGTTCATTCATCCGAAATG 717
RESULT 10
ADS62464
ID ADS62464 standard; cDNA; 720 BP.
XX
AC ADS62464;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #14451.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI, 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 38138; 122bp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 720 BP; 181 A; 166 C; 198 G; 175 T; 0 U; 0 Other;

Alignment Scores: 1,11e-114 Length: 720
Pred. No.: 1075.00 Matches: 206
Score: 93.74 Conservative: 18
Percent Similarity: 86.24 Mismatches: 15
Best Local Similarity: 87.44 Indels: 0
Query Match: 13 Gaps: 0
DB:

US-10-817-483-2 (1-239) x ADS62464 (1-720)

QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGGATCTGCGCTTAATTTTCGGTCCCACTTCACAGAAACACTCCAGCCCGGAGCT 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTTCGCCAGACAGCTGGCTTCCTTCCTTCGCTCGATCGGGGTCCAATGTTGCTCTCAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuValGlyThrThrArgLeuTyr 60
DB 121 CTGTCAACCGGAGGAGGAGCAACCAAGTGAAGAACTGAAGGAACGAGCGCTCATAC 180
QY 61 LeuAspAspArgProLeuValIleGlyIleIleThrAlaIleGlnAlaIleGlnArgLeu 80
DB 181 CTGTGATGATCGGCTCTGCTGTAAGGTTATCATCCGACCAAGCTCATGAAAGGCTG 240
QY 81 IleaIaGluValIleAsnHisGlnAlaIleGlyGlyLeuIleLeuGluGlyGlySerIle 100
DB 241 ATGGGGAGAGTGTATTAATTATGAGGCCACGCGGGCTTATTCCTGAGGAGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAAGTGCATGCGCAAGCAGTTATTTGAGTGCAGATTTTCGTTGGCATATT 360
QY 121 IleaTgaSngLleuAlaSpGluSerPheMetSerValAlaIleThrArgVallys 140
DB 361 ATTCGCCAGAGTTGACGAGACGAAAGACCTTCATGAACTGGCCAAAGCCAGATTAAAG 420
QY 141 GlnMetLeuArgProSerIleAglyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTGCTGCAGAGCCCTTCTATTATTCAGAACTGGTTGATCTTTGGAAA 480
QY 161 GlnProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCTTCGGCTGACGCCCCACTACTGAAAGATCGATGATATCGATATCCATGTTGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTACCCAGAACCAAGTCCATCCGATATGTCATTGACAGCTTGACGACATATGAGAGAT 600

XX Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; XX pathogen tolerance; pest tolerance; plant disease resistance; XX cell cycle pathway modification; plant growth regulator; XX homologous recombination; seed oil yield; protein yield; carbohydrate; XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan; XX bacterial polynucleotide; gene; ss. XX Bacteria. XX OS US2003233675-A1. XX PN 18-DEC-2003. XX PD 20-FEB-2003; 2003US-00369493. XX PF 21-FEB-2002; 2002US-0360039P. XX PR (CAOY/) CAO Y. XX PA (HINK/) HINKLE G J. XX PA (SLAT/) SLATER S C. XX PA (CHEN/) CHEN X. XX PA (GOLD/) GOLDMAN B S. XX P1 Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS; XX DR WPI; 2004-061375/06. XX PT New recombinant DNA construct comprising a promoter positioned to provide PT for expression of a polynucleotide encoding a polypeptide from a PT microbial source, useful for producing plants with improved properties. XX PS Claim 1; SEQ ID NO 38549; 122pp; English. XX XX CC The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plants with CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests, CC increased resistance to plant disease, better growth rate by modification CC of the cell cycle pathway with plant growth regulators, increased rate of CC homologous recombination, modified seed oil or protein yield and/or CC content, improved yield by modification of carbohydrate, nitrogen or CC phosphorus use and/or uptake, by modification of photosynthesis or by CC providing improved plant growth and development under at least one stress CC condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polynucleotide used in CC the scope of the invention. Note: The sequence data for this patent did CC not form part of the printed specification but was obtained in electronic CC format from USPTO at seqdata.uspto.gov/sequence.html. XX SQ Sequence 720 BP; 181 A, 166 C, 198 G, 175 T, 0 U, 0 Other; XX

Alignment Scores:
Pred. No.: 1.11e-114 Length: 720
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) x ADS62875 (1-720)

OY 1 MetaBleuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleala 20

DB 1 ATGATCTGCGCTTATTTTGGTCCAACTTCACAGGAAGACGTCGACCCGGAGCTT 60
OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTGGCCAGCAGACTGGGCTTCCTGCTGGCTGGATCGGGGTCCAAATGTTGCTCTG 120
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTy 60
DB 121 CTGTCAACCGGAAGCGACGACCAACAGTGAAGAACTGAAGAAACGAGCGCTGTATAC 180
OY 61 LeuAspArgProLeuValLysGlyTlleThrAlaLysGlnAlaHisGlnArgLeu 80
DB 181 CTGTATGATCGGCTCTGAGTAAGGATATCATCGACGACCAAGCTCATATAAAGGCTG 240
OY 81 IleAlaGluValHisAsnHisGlnValLysGlyGlyLeuLeuGluGlySerIle 100
DB 241 ATGGGGGAGGTGTATATATATATGAGCCACGCGGGCTTATTCTTGAGGAGATCTATC 300
OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTyrPasnAlaAspPheArgTyrHisIle 120
DB 301 TCGTTGCTCAAGTGCATGGCGCAAGCAGTTATGAGATGCGGATTTTCGTTGCATATT 360
OY 121 IleArgAsnGluLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
DB 361 ATTCGCACAGATTAGCAGACGAGGACCTTCATGAACTGCGCAAGGCCAGAGTTAAG 420
OY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTyrArg 160
DB 421 CAGATGTTACGCCCTCGCTGAGGCTTCTTATATATCAAGATGTTGATGTTGGAA 480
OY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCCTCGGCTGAGGCGCCATCTGAAGAGATCGATGATATGCCATGTTGTTT 540
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GTTACCCAGAACCAATCATCCGATATGCTATTCAGCTTGACGACGATATGAGAGAT 600
OY 201 LysLeuIleHisGlyTlleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
DB 601 AAGTTGATTCATGGATGCTCTCAGAGATATCTCATCCATCGCGCCGACAAACAGAA 660
OY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGlnGlyProProPheArgMet 239
DB 661 TTCCCTCGAGTTAAACGACGCGCTTACGACGAGATTCGAAGTCATCCATTCGAATG 717

RESULT 13
ADT62691
ID ADT62691 standard; DNA; 723 BP.
XX ADT62691;
XX 13-JAN-2005 (first entry)
DT 13-JAN-2005 (first entry)
XX DE DNA encoding A. tumefaciens isopentenyl transferase (IPT).
XX DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
KW expression cassette; transgenic plant; transgenic;
KW isopentenyl transferase; IPT; ds.
XX KM Agrobacterium tumefaciens.
XX OS WO2004092390-A2.
XX PN 28-OCT-2004.
XX PD 09-APR-2004; 2004WO-US011000.
XX PF 09-APR-2003; 2003US-0461459P.
XX PR (MONS) MONSANTO TECHNOLOGY LLC.
XX PA

PI Gilbertson L, Krieger E, Zhang W, Ye X;
XX WPI; 2004-758349/74.
XX
PT New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
PT first border region linked to a transgene linked to an Agrobacterium Ti
PT plasmid second border region, useful for enhancing production of
PT transgenic plants.
XX
PS Example 1; SEQ ID NO 2; 77bp; English.
XX
CC The present invention relates to a DNA plasmid comprising a transfer DNA
CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
CC to at least one transgene linked to an Agrobacterium Ti plasmid second
CC border region, and located in the DNA plasmid outside of the T-DNA is a
CC plant expression cassette comprising a plant cell non-lethal negative
CC selectable marker gene linked to a vector backbone DNA. Also disclosed
CC are a method for enhancing the selection of transgenic plants that do not
CC contain vector backbone DNA, a method for reducing the copy number of a
CC transgene in a plant cell, and a transgenic plant produced by the method.
CC The DNA plasmid comprises the expression cassette comprising a promoter
CC that functions in plant cells operably linked to a plant cell non-lethal
CC negative selection marker gene. The promoter is a constitutive promoter.
CC The promoter expresses the linked non-lethal negative selection marker
CC gene product in tissue culture during plant regeneration. The plant cell
CC non-lethal negative selectable marker gene comprises a plant hormone
CC biosynthetic pathway gene, degradative gene, biosynthetic pathway
CC substrate-diverting gene or signaling gene, or metabolic interference
CC gene. The transgene is a plant positive selectable marker gene selected
CC from antibiotic resistance and herbicide resistance. The transgene
CC comprises a transgene of agronomic interest. The plant hormone
CC biosynthetic pathway gene is selected from gibberellic acid pathway
CC genes, cytokinin pathway genes, auxin pathway gene, ethylene pathway
CC genes, and abscisic acid pathway genes. The plasmid is useful for
CC enhancing the production of commercially viable transgenic plants. The
CC present sequence represents DNA encoding Agrobacterium tumefaciens
CC isopenentenyl transferase (IPT) enzyme. This sequence is used as a non-
CC lethal negative selectable marker.
XX
SQ Sequence 723 BP; 183 A; 166 C; 198 G; 176 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,12e-114 Length: 723
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 13 Gaps: 0
US-10-817-483-2 (1-239) x ADR62691 (1-723)
QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLeuSerThrAlaIleAla 20
DB 1 ATGATCTGCGCTCTAATTTTCGGTCCACTGACAGAAAGACGTGACCGGGTAACT 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTGCGCCAGCAGACGTGGGCTTCCTCACTTCCTGCGATCGGGTCCAAATGTTGCTTAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThrArgLeuTyr 60
DB 121 CTGTCAACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGAACGCGCTTAAAC 180
QY 61 LeuAspArgProLeuValIleuSerGlyIleIleThrAlaLysGlnAlaIleGlnArgLeu 80
DB 181 CTGTGATGATCGGCTCTGTTGAAGGGTATCATCGACGCCAAGCAAGCTCATGAAGGCTG 240
QY 81 IleAlaGlnValIleAsnHisGlnAlaLysGlyGlyLeuIleLeuGlnGlySerIle 100
DB 241 ATGGGGAGGGTATTAATTAATTAAGGCCACCGCGGGCTTATTTCTTGAAGGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120

DB 301 TCGTGTCAAGTCATGCGCGCAAGACGATTATGAGTGGGATTTTCGTGGCATATT 360
QY 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaIleThrArgValIle 140
DB 361 ATTGGCAGCAGGTTAGAGACGAAAGAGACCTTCATGTAACTGGCCAAAGGCCAGATTAA 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTGCTGCGAGGCTTCTATTTCACAGAGTTGGTGTGATTTGGAAA 480
QY 161 GlnProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCTCGGCTGAGGCCCATCTGAAGATCATGATGATGATGATGATGATGATGATGAT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
DB 541 GCTGCGCAGAACCCAGATCACATCCGATATGTATGAGCTTGACGAGATATGAGAGAT 600
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnLys 220
DB 601 AAGTTGATTCATGGATTCCTCAGAGATATCTTCATGACGCCCAAGAAACAGAAA 660
QY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB 661 TTCCTCGAAGTTACGACGCGCTTACAGACGATTCGAAAGTCAATTCGATG 717
RESULT 14
ADR42934
ID ADR42934 standard; DNA; 723 BP.
XX
AC ADR42934;
XX
DT 18-NOV-2004 (first entry)
XX
DE IPT-like structural gene #1.
XX
KW Abscission zone; apical meristem; Plant Growth Regulant; Gene Therapy;
KW A6; abscission zone promoter; IPT; isopenyl transferase; de.
XX
OS Unidentified.
XX
PN WO2004074442-A2.
XX
PD 02-SEP-2004.
XX
PF 13-FEB-2004; 2004WO-US004499.
XX
PR 14-FEB-2003; 2003US-0447833P.
XX
PA (MONSANTO TECHNOLOGY LLC.
XX
PI Bhat DG, Deng W, Eilers RJ, Nelson DE, Tennessee DJ;
XX WPI; 2004-635562/61.
XX
PT New polynucleotides comprising a plant promoter that directs its
PT transcription into abscission zone(s), root, pod, wall, apical meristem,
PT or flower of plants, useful for producing a plant having increased yield
PT or agronomic trait.
XX
PS Claim 21; SEQ ID NO 16; 63bp; English.
XX
CC The present invention relates to an isolated polynucleotide comprising a
CC plant promoter directing transcription of an operably linked
CC polynucleotide in at least one of the tissues selected from abscission
CC zone, root, pod, wall, apical meristem, and flower of plants. The
CC polynucleotides and methods are useful for producing a plant having
CC increased yield or a trait of agronomic interest when compared to a non-
CC transformed plant of the same genotype. The present sequence represents a
CC IPT-like structural gene. The sequence data for this patent is not
CC represented in the printed specification but was obtained in electronic
CC format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm.

Sequence 723 BP, 182 A, 166 C, 199 G, 176 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	7,24e-114	Length:	723
Score:	1068.00	Matches:	205
Percent Similarity:	93.3%	Conservative:	18
Best Local Similarity:	85.8%	Mismatches:	16
Query Match:	86.8%	Indels:	0
DB:	13	Gaps:	0

US-10-817-483-2 (1-239) x ADR42934 (1-723)

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QY      1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB      1 ATGGATCTGGCGTCTAATTTTCGGTCCAACTTCGACAGAAACGTCGACCCGCGTAGCT 60

QY      21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
DB      61 CTGGCCACAGACATGGGCTTCAGTCTTCGCTCGATCGGGGTCGCAATGTTGTCTCTCG 120

QY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB      121 CTGTCAACCGGAGAGGGAGCAGCAACAGTGAAGAACTGAAGAAACGACCGCTCATAC 180

QY      61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB      181 CTTGATGATCGGCTCTGGTGAAGGGTATCATCGCAGCCAAACCAAGCTCATGAAGGCTG 240

QY      81 IleAlaGluValHisAsnHisGluValLysGlyLysGlyLeuIleLeuGlnGlyLysSerIle 100
DB      241 ATGGGGGGGGGTATATATATATAGAGGCCAGCGGGCTTATCTTGAGGAGAGATCTATC 300

QY      101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTTPAsnAlaAspPheArgTrpHisIle 120
DB      301 TCGTTGCTCAAGTCATGCGCCGCAAGCAAGTTATGGAGCGCGATTTTCGTTGCGCATAT 360

QY      121 IleArgAsnGlnLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
DB      361 ATTCGCCACGAGTTCAGACAGACAGACCTTCATGAAAGTGGCCAAAGCCAGAGTTAAG 420

QY      141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTyrArg 160
DB      421 CAGATGTTACGCCCTCGCGACAGCCCTTTTATTTATTCAAAGATGGTGTATCTTTGGAAA 480

QY      161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB      481 GAGCGCTCGGCTGAGGCCCATTACTGAAGAGATCGATCGATATCGATATCCATGTTGTTT 540

QY      181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB      541 GCTACCCAGAACCAAGATCATCTCGATATGCTATTGACGCTTGACGCAAGATATGAGGAT 600

QY      201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
DB      601 AAGTTGATTCATGGGATCGCTCAGAGATTCATCTCATTCAGTCACGCCGAAACAAACGAAA 660

QY      221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB      661 TTCCCTCGAGTTAACGCAAGCCGCTTAACAGCGATTCGAAGTCATCTCGAATG 717

RESULT 15
ID      ADR42936 standard; DNA; 723 BP.
XX      AC      ADR42936;
XX      DT      18-NOV-2004 (first entry)
XX      DE      IPT-like structural gene #2.
XX      KW      abscission zone; apical meristem; Plant Growth Regulant; Gene Therapy;
KW      A6; abscission zone promoter; IPT; isopentenyl transfease; ds.

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OS      Unidentified.
XX      XX      WO2004074442-A2.
XX      XX      02-SEP-2004.
XX      PD      13-FEB-2004; 2004WO-US004499.
XX      PF      14-FEB-2003; 2003US-0447833P.
XX      PR      (MONS ) MONSANTO TECHNOLOGY LLC.
XX      PA      Bhat DG, Deng M, Eilers RJ, Nelson DE, Temessen DJ;
XX      PI      WPI; 2004-635562/61.
XX      DR      New polynucleotides comprising a plant promoter that directs its
PT      transcription into abscission zone(s), root, pod, wall, apical meristem,
PT      or flower of plants, useful for producing a plant having increased yield
PT      or agronomic trait.
XX      PS      Claim 21; SEQ ID NO 18; 63pp; English.
XX      CC      The present invention relates to an isolated polynucleotide comprising a
CC      plant promoter directing transcription of an operably linked
CC      polynucleotide in at least one of the tissues selected from abscission
CC      zone, root, pod, wall, apical meristem, and flower of plants. The
CC      polynucleotides and methods are useful for producing a plant having
CC      increased yield or a trait of agronomic interest when compared to a non-
CC      transformed plant of the same genotype. The present sequence represents a
CC      IPT-like structural gene. The sequence data for this patent is not
CC      represented in the printed specification but was obtained in electronic
CC      format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm.
XX      XX

SQ      Sequence 723 BP, 182 A, 166 C, 199 G, 176 T, 0 U, 0 Other;

Alignment Scores:
Pred. No. : 7,24e-114 Length: 723
Score: 1068.00 Matches: 205
Percent Similarity: 93.3% Conservative: 18
Best Local Similarity: 85.8% Mismatches: 16
Query Match: 86.8% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) x ADR42936 (1-723)

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DB      1 ATGGATCTGGCGTCTAATTTTCGGTCCAACTTCGACAGAAACGTCGACCCGCGTAGCT 60

QY      21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
DB      61 CTGGCCACAGACATGGGCTTCAGTCTTCGCTCGATCGGGGTCGCAATGTTGTCTCTCG 120

QY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB      121 CTGTCAACCGGAGAGGGAGCAGCAACAGTGAAGAACTGAAGAAACGACCGCTCATAC 180

QY      61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB      181 CTTGATGATCGGCTCTGGTGAAGGGTATCATCGCAGCCAAACCAAGCTCATGAAGGCTG 240

QY      81 IleAlaGluValHisAsnHisGluValLysGlyLysGlyLeuIleLeuGlnGlyLysSerIle 100
DB      241 ATGGGGGGGGGTATATATATATAGAGGCCAGCGGGCTTATCTTGAGGAGAGATCTATC 300

QY      101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTTPAsnAlaAspPheArgTrpHisIle 120
DB      301 TCGTTGCTCAAGTCATGCGCCGCAAGCAAGTTATGGAGTGGCGATTTTCGTTGCGCATAT 360

QY      121 IleArgAsnGlnLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
DB      361 ATTCGCCACGAGTTACAGACAGAAAGACCTTCATGAAAGTGGCCAAAGCCAGAGTTAAG 420

```

[illegible]

Search completed: June 26, 2006, 19:53:26
Job time : 655 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 19:46:01 ; Search time 4446 Seconds
(without alignments)
4509.015 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230

Sequence: 1 MDRLIFGPTCTGKTSTAIA.....KPLVGAATVAFAFGSPPRM 239

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-O=/abs/ABSSMB spool/US10817483/runat 26062006 142748 18815/app query.fasta_1
-DB=EST -OPMT=fastad -SUPERX-p2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human4.0.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=PCT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs803p
-USER=US10817483 @CGN 1 1 9528 @runat 26062006 142748 18815 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124	10.1	883	14	DU740683
2	115	9.3	763	5	CK714752 LECAD01B1
3	112.5	9.1	692	3	BO972287 OHC3b07.Y
4	112	9.1	656	8	CV005106 pam01-11m

5	111.5	9.1	886	10	DT209523 JGI_CAA51
6	109.5	8.9	867	10	DT280070 JGI_CAAV9
7	107	8.7	1769	6	AK166259 Mus_muscu
8	106.5	8.7	831	12	CC391172 CC391172
9	106.5	8.7	916	12	CC391169 PNHCV57TD
10	105.5	8.6	1113	10	CC391169 PNHCV57TD
11	104.5	8.5	876	10	DM596236 CGX123-E1
12	103	8.4	768	13	DT179124 JGI_ANN04
13	102.5	8.3	871	8	CG218570 OA_BBA003
14	102.5	8.3	881	10	DT267881 DT267881
15	102	8.3	818	5	CK603491 CK603491
16	102	8.3	1951	6	AK010176 AK010176
17	102	8.3	2061	6	AK003556 AK003556
18	101.5	8.3	756	10	DT151607 DT151607
19	101.5	8.3	816	12	CC624173 CC624173
20	101	8.2	2734	6	AK154256 AK154256
21	100.5	8.2	1346	5	CD502446 CD502446
22	99.5	8.1	845	9	CK500862 CK500862
23	99.5	8.1	857	10	DM648982 DM648982
24	99.5	8.1	1150	10	DM664662 DM664662
25	98.5	8.0	739	10	DT819055 DT819055
26	98.5	8.0	741	4	EX733862 EX733862
27	98.5	8.0	833	9	CK425315 CK425315
28	98.5	8.0	855	9	CK970110 CK970110
29	98.5	8.0	858	9	CK911134 CK911134
30	98.5	8.0	888	9	CK896821 CK896821
31	98.5	8.0	1056	10	DM646720 DM646720
32	98.5	8.0	1064	10	DM675840 DM675840
33	98.5	8.0	1133	10	DM664631 DM664631
34	98.5	8.0	1340	10	DN700914 DN700914
35	98.5	8.0	1353	10	DT968333 DT968333
36	98.5	8.0	1442	10	DT970650 DT970650
37	98	8.0	663	2	B1249363 B1249363
38	98	8.0	675	2	BS973165 BS973165
39	97.5	7.9	765	9	CK926825 CK926825
40	97.5	7.9	852	4	BK625184 BK625184
41	97	7.9	729	2	BS519462 BS519462
42	97	7.9	1074	10	DM664632 DM664632
43	97	7.9	1738	6	AK150081 AK150081
44	97	7.9	1751	6	AK152329 AK152329
45	97	7.9	1768	6	AK088824 AK088824

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
DU740683	APK1584.g2	HF70_10-07-02 uncultured marine microorganism	DU740683	DU740683.1	GI:85750517	GSS	uncultured marine microorganism HF70_10-07-02	1 (bases 1 to 883)	DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J., Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W. and Karl,D.M.	Comparative genomics reveals ecological trends in stratified microbial communities in the ocean's interior	Science (2006) In Press	Contact: Susan Lucas, Alex Copeland, Sam Plickuck, Alla Lapidus, Kerrie Barry, Tijana Glavanadeliro, David Bruce, Paul Richardson and Edward Delong
US DOE Joint Genome Institute	US DOE Joint Genome Institute	2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA	Tel: 617-253-5271	Fax: 617-253-2679	Email: PMRichardson@lbl.gov; delong@mit.edu	Sample Date: 10/7/2002	Coordinates: 22.45 N, 158 W	Depth 70 m				

Qy 109 SerArgTYrTPasnaAlaaspPheargTrpHisIleIleArgAsnGluLeuAlaAspGlu 128
|||
Db 520 CAGCGTCTGGTGTGATGATGATTCCTTCACGGCCCTACTCAACGTAAGAA 579
|||
Qy 129 GluSerPheMetSerValAlaIlyThrArgValIySgImeLeuArgProSerIaGly 148
|||
Db 580 GAG-----AGATCTTAGATAGTACTGCATAA 606
|||
Qy 149 LeuSerIleIleGlnGluLeuValGlnLeu-----TPArg----- 160
|||
Db 607 GGAACATAAGATGAAGAGCTTATAGATTGTGATGAGAGAAAGCTGCAGAGAAACA 666
|||
Qy 161 -----GluProArgLeuArgProIle--LeuGlnGly 170
|||
Db 667 GCTCTTTGCGTCAAGTGAAGTGAACCTGTGCTCCGTGGCTTGGAAGGT 717
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RESULT 3
BO972287 692 bp mRNA linear EST 21-AUG-2002
LOCUS QHC3b07.y9.ab1 OH ABCDI sunflower RHA801 Helianthus annuus cDNA
DEFINITION BO972287
ACCESSION BO972287
VERSION BO972287.1 GI:22389810
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L.,
Lin, H., Van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
UNPUBLISHED (2002)
CONTACT: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmndson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: QHC3 row: b column: 07.
Location/Qualifiers
FEATURES
Source
1..692
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RHA801"
/db_xref="taxon:4232"
/clone="QHC3b07"
/lab_host="E.Coli1"
/clone_id="OH ABCDI sunflower RHA801"
/note="Vector: pBRCDNA5f1AB; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=hulls
TAG_LIB=OH ABCDI sunflower RHA801
TAG_SEQ=GTAGTCGGG"
ORIGIN
Alignment Scores: 0.0481 Length: 692
Pred. No.:

Score: 112.50 Matches: 49
Percent Similarity: 42.1% Conservative: 36
Best Local Similarity: 24.3% Mismatches: 94
Query Match: 9.1% Indels: 23
DB: 3 Gaps: 6
US-10-817-483-2 (1-239) x BO972287 (1-692)
Qy 5 LeuIlePheGlyProThrCysThrGlySerThrSerThrAlaIleAlaLeuAlaGlnGln 24
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Db 86 CTATACGTAAGTAGAGAGAGAAACCGTAAACCGACACTAGCATGATAGCCGACAG 145
|||
Qy 25 ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrGly 44
|||
Db 146 GCGAAGGTCCCGGTGTGAGAGTTAAGGCTCAACGATTAGAGCGCGGCTTAGGGTGGC 205
|||
Qy 45 SerGlyArgProThrValGlnGluLeuIySgIlyThrThrArg----- 58
|||
Db 206 CAGAGTCATCCACACGTTAGAGACTGTTCCAAACGCCGAGATCTGCGCCCTGATC 265
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Qy 59 LeuTYrLeuAspAspArgProLeuValIySgIly-----IleIleThrAla 73
|||
Db 266 ATATTGTGGAAGATTGTTGATCTCTTGCTGTAAACGAGGAGATTATACATCTAA 325
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Qy 74 LysGlnAlaHisGlu-----ArgLeuIleAlaGluValHisHisGlnAla 89
|||
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|||
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Qy 109 SerArgTYrTPasnaAlaaspPheargTrpHisIleIleArgAsnGluLeuAlaAspGlu 128
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Qy 129 GluSerPheMetSerValAlaIlyThrArgValIySgImeLeuArgProSer----- 146
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Db 506 GAGAGAAATCACTCAATCGCT-----GCGAAGAAAGAACTGATGATCGACCTTATT 556
|||
Qy 147 -----AlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTPArgGluProArgLeu 164
|||
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Qy 165 ArgProIleLeuGlnGlyIleAspGlyTYrArgTYrAlaLeuLeuPheAlaThrGlnAsn 184
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Db 677 GAACCTT 682
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LOCUS CUV005106 656 bp mRNA linear EST 18-AUG-2004
DEFINITION pam01-1lms3-e09 Pam01 Persea americana cDNA clone pam01-1lms3-e09
5', mRNA sequence.
ACCESSION CUV005106
VERSION CUV005106.1 GI:51364329
KEYWORDS EST.
SOURCE Persea americana (avocado)
ORGANISM Persea americana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
Persea.
REFERENCE
AUTHORS 1 (bases 1 to 656)
dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
Opdenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
Leebens-Mack, J., Landherr, L., Ilut, D. and Wall, K.
Generation of ESTs from early flower buds of Persea americana
UNPUBLISHED (2003)
CONTACT: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory

Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwb3@psu.edu or jh110@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (<http://pgn.cornell.edu>)
Plate: pam01-1lms3 row: a column: 09
Seq primer: M13F.

FEATURES
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1..656
Location/Qualifiers
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/db_xref="taxon:3435"
/clone="pam01-1lms3-a09"
/tissue_type="flower buds"
/dev_stage="12-20 mm buds"
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/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; This is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at <http://fgp.bio.psu.edu>"

ORIGIN

Alignment Scores:

Pred. No.: 0.0509 Length: 656
Score: 112.00 Matches: 50
Percent Similarity: 43.0% Conservative: 30
Best Local Similarity: 26.9% Mismatches: 72
Query Match: 9.1% Indels: 34
DB: 8 Gaps: 7

US-10-817-483-2 (1-239) x CV005106 (1-656)

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Db 166 GCTAAGGTGCTCTGTGTAAGCTCGTCAGCTGAGAGGCTGAGACTCTGGGTTG 225
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Qy 45 SerGlyArgProThrValGlnGluLeuLeuGlyThrThrArg----- 58
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Db 226 CAAAGTCTTGAATGTGAAGAGCTGTTTCAACAGCAGGAGATTGGCCACCACTATA 285
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Qy 59 LeuTyrlleuAspAspArgProLeuValLysGly-----IleIleThrAla 73
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Db 346 AACACGAGCAGCATGAAGCATTTATCAACCACTCTTGTGGAACCTTGATGGGTTTGAGAAA 405
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Qy 90 LysGlyGlyLeuIleLeuGlnGlyGlySerIleSerLeuLeuArgCys---MetAlaGln 108
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Db 406 CAAAGTGGGGTGTGTTTAATGGCCACCAAGAAATTTAAAGCAATTGACCAAGGCTTTG 465
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Qy 109 SerArgTyrlPAsnAlaAspPheArgTrpHisIleIleArgAsnGluLeuAlaAspGlu 128
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Db 466 AAAGCAGCAGGCGCGATGATGAATTCATCTTCAACCGCCCACTCAAGATGAAGA 525
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Qy 129 GluSerPheMetSerValAlaLysThrArgValLysGlnMetLeuArgProSerAlaGly 148
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Db 526 GAG-----AAGATTTTAAGATAGACAGCAAC 552

Qy 149 LeuSerIleIleGlnLeuValGlnLeu-----TrpArgGlu----- 161
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Db 553 GAAACCAATGATGATGAATCATATTGTTAGTAAATTGAGAAAGCTTCAGAGAAAACA 612
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Qy 162 ProArgLeuArgProIle 167
|||
Db 613 GCTCTTTTACCGCCTGTA 630
|||

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UNPUBLISHED (2005)

Other ESTs: UGI_CAS16003.rev

Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 5600

Fax: 925 296 5710

Email: cdna@jgi-psf.org

CDNA Library Preparation: DOE Joint Genome Institute:

<http://www.jgi.doe.gov>

DNA Sequencing: DOE Joint Genome Institute:

Naming Conventions: EST name is generated by the concatenation of

the UGI Clone Id and the direction of sequencing. The suffix 'fwd'

indicates a forward sequencing read of the insert. It does not

necessarily reflect the orientation of the insert.

Plate: CAAS 0165 row: e column: 18

High quality sequence stop: 757.

FEATURES

source

1..886
Location/Qualifiers

/organism="Pimephales promelas"

/mol_type="mRNA"

/db_xref="taxon:90988"

/clone="CAS16003"

/tissue_type="brain"

/clone_lib="CAAS Pimephales promelas brain 7-8 month

adults, males and females pooled (H)"

/note="Vector: pCMVSPORT6; The library was made from dT

primed cDNA and cloned into Invitrogen vector pCMVSPORT6.

Poly A RNA were primed with an oligo dT primer (5'-

GACTAGTTCAGATCGAGCGCGCCCTTTTCTTTTCTTTT-3') ligated

to a SalI adapter (5'-TCGACCCAGCGGTCCG and 5'-

CGGACGGGTGGG) and digested with NotI. cDNA was size

selected using 1.1% agarose gel electrophoresis (L

~0.5-1.2k, M ~1.2-2.5k, H ~2.5k) then ligated into NotI

and SalI digested pCMVSPORT6 vector. The work was done at

DOE Joint Genome Institute."

ORIGIN

Alignment Scores:

Pred. No.: 0.0897 Length: 886
Score: 111.50 Matches: 52
Percent Similarity: 42.5% Conservative: 38
Best Local Similarity: 24.5% Mismatches: 75
Query Match: 9.1% Indels: 47
DB: 10 Gaps: 13

US-10-817-483-2 (1-239) x DT209523 (1-886)

Oy		33	AspaValgInGncYcSvProGlneUeSerThrgYserGIYarPProThrValGIuGLn	52
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Oy		53	LeuYsgIYThrThrArgLeuTYrleuAasp-----ArgProLeuVallysgIyle	70
Db		190	CTGTACACCGAGACGAAGGTGTTTCTTGAGAACAACGTCGCCGCACTGTTCAAAGAATC	249
Oy		71	IleThraIalYsGlnAlaHisGIlaYrGuileuIleaGIuValHIsAsnHis-	87
Db		250	CTG-----GACTCTGAAGAGAAAGTTTTGGTATGTATCACAGATTACTGGGAGAG	300
Oy		88	GIuaIalYsGIYGLYleuIlenuGIuGIyserIleserleuYArGYSMeLa	107
Db		301	TACAGCAAAGCGCGCTGAGTACATGAT-----TGCTTA-----	333
Oy		108	GlnserArGYrTYrTpAsnAlaasPheArGrTrpHisIleIearGAsnGIuLeuAlaap	127
Db		334	---TACAGATATCCTGACACACAGTTC-----ATTAGAACAACAGCTGACGAA	381
Oy		128	GIuIGuSerPheMetSerValAlalySthrArgValYsGlmMetLeuArGPsoSerLa	147
Db		382	GCTGACCTGCAGTACGATATGAGAGATGAGACATGAACGAGCCGTTA-----	429
Oy		148	GIYeuSerIleIleGIuGIuLeuValGIuLeuTParG-----GluProArg	163
Db		430	---ATGAGATCTGGAGACCTTGCACTGCACATGTGCCGAAGTTATATTTGAGCT--	483
Oy		164	LeuArGPProIleLeuGIuGIYleaspeLyTYrArGYralaleuLeuPheaIathrGln	183
Db		484	CTTCAACCCATGCTCATCGGGATG-----CTTCTGAAGAAGATCAAG	525
Oy		184	AseGnIIethrProaspMetleuGIuGIuLeuAspAlaasPmetGIuAsnLYsleuIle	203
Db		526	AACGAC-----CGATGTGGGAGAGACCCAATCAGAAAATAATC	564
Oy		204	HIegIYlealagIngluPheleuIleHisAlaArGsGlnGIuGIuLYsPheProku	223
Db		565	CACGGGGTTATCAATCCTTT---CTTATGTGAACAATCAAGAAAAAGTTTCTCTA	621
Oy		224	ValGIalathrAlaValaGIuAlaPheGIuGIYPro	235
Db		622	-----AAGTTTATCAGAGATCTTTGAGGGCCG	651
RESULT 6				
DT280070				
LOCUS				
DEFINITION	JGI CAAV9004.fwd cDNA Pimphales promelas testes 7-8 month adults,			
	males and females pooled (H) Pimphales promelas cDNA clone			
	CAVA9004 5', mRNA sequence.			
ACCESSION	DT280070			
VERSION	DT280070.1			
KEYWORDS	EST.			
SOURCE	Pimphales promelas			
ORGANISM	Pimphales promelas			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Actinopterygii; Neopterygii; Teleostei; Osteichthyes;			
	Cypriniformes; Cyprinidae; Pimphales.			
REFERENCE	1 (bases 1 to 867)			
AUTHORS	Richardson,P., Lucas,S., Rokhsar,D., Dettler,J.C., Ng,D.C.,			
	Brockstein,P. and Lindquist,E.A.			
	DOE Joint Genome Institute Pimphales promelas EST project			
	Unpublished (2005)			
TITLE	Other_ESTs: JGI_CAAV9004.rev			
JOURNAL	Contact: Lindquist,E.A., Richardson,P.			
COMMENT	DOE Joint Genome Institute			
	2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
	Tel.: 925 296 5600			
	Fax: 925 296 5710			
	Email: cdna@jgi-psf.org			
	cDNA library Preparation: DOE Joint Genome Institute:			
	http://www.jgi.doe.gov			

FEATURES			
SOURCE			
<p>DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov</p> <p>Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix ".fwd" indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.</p> <p>Plate: CAAV 0093 row: h column: 19</p> <p>High quality sequence stop: 782.</p> <p>Location/Qualifiers</p>			
1..867	/organism="Pimephales promelas"		
	/mol_type="mRNA"		
	/db_xref="taxon:90988"		
	/clone="CAAV9004"		
	/issue_type="testis"		
	/clone_lib="CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (H)"		
	/note="Vector: pCMVSPORT6; The library was made from DT primed cDNA and cloned into Invitrogen vector pCMVSPORT6. Poly A RNA were primed with an oligo dT primer (5'-GACTGTTGATGATCGAGCGCCGCTTTTCTTTT-3') ligated to a SalI adapter (5'-TCGACCAAGCGGTCCG and 5'-CCGACCGGTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L ~0.5-1.2kb, M ~1.2-2.5kb, H ~2.5kb) then ligated into NotI and SalI digested pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute."		
ALIGNMENT SCORES:			
Pred. No.:	0.148	Length:	867
Score:	109.50	Matches:	52
Percent Similarity:	42.0%	Conservative:	57
Best Local Similarity:	24.5%	Mismatches:	76
Query Match:	8.9%	Indels:	47
DB:	10	Gaps:	13
US-10-817-483-2 (1-239) x DT280070 (1-867)			
QY	33	AsparGValGInCysEcysProGInIleuSerThrGlySerGlyArgProThrValGluGlu	52
DB	293	GACCGCTTCTCAGACACTATACGCGCTGTGTGCGATATCCGAGCGCTTAAGGGAAAG	352
QY	53	LeuLysGlyThrThrArgLeuTyrIleuAsp-----ArgProLeuValLysGlyIle	70
DB	353	CTGTACACCGAAGCAAGAGTGTCTTGAGAACACACGTCGCGAGCTGTTCAGAGAGATC	412
QY	71	IleThrAlaLysGlnAlaHisGluLysArgLeuIleAlaGluValHisAsnHis-----	87
DB	413	CTG-----GAGCTGAAGAGAAAGGTTTGGTATGATGATTCACAGATCTGGAGAG	463
QY	88	GluAlaLysGlyGlyLeuIleLeuGluGluGlySerIleSerLeuLeuArgCysMetAla	107
DB	464	TACAGCAAAAGTGCTGAGTACATGAT-----TGCTTA-----	496
QY	108	GlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIleIleArgAsnGluLeuAlaAsp	127
DB	497	---TACAGATACCTGAACACACAGATTC-----ATTAAAGAGAACAGCTGACCGAA	544
QY	128	GluGlnSerPheMetSerValAlaLysThrArgValLysGlnMetLeuArgProSerAla	147
DB	545	GCTGACCTCGATACGATATGAGAGAGTGAACATGAACGAGCCGTTA-----	592
QY	148	GlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg-----GluProArg	163
DB	593	---ATGAGATCGGAGAGCTTGCACTGACACATGTGGCGGAAGTTAATGATTGAGCTT	646
QY	164	LeuArgProIleLeuGluGlyIleAspLysTyrArgTyrAlaLeuLeuPheAlaTrpGln	183
DB	647	CTTCAAACCATCTCATCGGGATG-----CTTCGAAGAAGATCAAG	688
QY	184	AsnGlnIleThrProAspMetLeuLeuGlnIleuAspAlaAspMetGluAsnLysLeuIle	203
DB	689	AACGAC-----CGAGTGTGGGAGACCCCAATCAAGAAATCAATC	727

Oy	204	HisclytllaagIngluPheLeuIleHisAlaArgaGIngluInLysPheProIeu	223
		::: ::: :::	
Db	728	CACGGCGTTATCAACTCCTT---GTTCATGTTCAGAACATACAGANAAGTTCCCTCN	784
Oy	224	ValGIyAlatrHrAlaValaGluaLaPheInGlyPro	235
Db	785	-----AAGTTTTATCAGAGAATTCTTGAGGGCCGC	814
RESULT 7			
AKI66259			
LOCUS			
DEFINITION	AKI66259	1769 bp mRNA linear HTC 21-SEP-2005	
	Mus musculus mammary gland RCB-0526 Ygc-M(CA) cDNA, RIKEN		
	full-length enriched library, clone:6830026C17 product:hypothetical		
	Alanine-rich region profile containing protein, full insert		
	sequence.		
ACCESSION	AKI66259		
VERSION	AKI66259.1 GI:74147543		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
	Sciurognathi; Muridae; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to		
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes		
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS	11042159		
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,		
TITLE	Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,		
JOURNAL	Sunji, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,		
PUBMED	Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K.,		
REFERENCE	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M.,		
AUTHORS	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
TITLE	Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.		
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format		
PUBMED	sequencing pipeline with 384 multicapillary sequencer		
REFERENCE	Genome Res. 10 (11), 1757-1771 (2000)		
AUTHORS	11076861		
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS	4		
	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,		
	Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, O., Fukuda, S.,		
	Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,		
	Saito, T., Okazaki, Y., Gotojohri, T., Bono, H., Kasukawa, T., Saito, R.,		
	Kadote, K., Matsuda, H., Asuburner, M., Batalov, S., Casavant, T.,		
	Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,		
	Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, T., Pesole, G.,		
	Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M.,		
	Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,		
	Baldarelli, R., Barsh, G., Blake, J., Bofield, D., Bojunga, N.,		
	Carninci, P., de Bonaldo, M.F., Brownstein, M.J., But, C.,		
	Fletcher, C., Fujita, M., Gariboldi, M., Gustinchich, S., Hill, D.,		
	Hochmann, M., Hume, D.A., Kamuya, M., Lee, N.H., Lyons, P.,		
	Machinomi, L., Mashima, J., Mazzarelli, J., Mommaerts, P.,		
	Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,		
	Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,		
	Toyo-Oka, K., Wang, K.H., Weitz, C., Whiteaker, C., Wilming, L.,		
	Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.		
	and Hayashizaki, Y.		
CONSRM	RIKEN Genome Exploration Research Group Phase II Team and the		
	FANTOM Consortium		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
PUBMED	11217851		

CONSRMT TITLE	REFERENCE AUTHORS
CONSRMT TITLE	REFERENCE AUTHORS
JOURNAL PUBMED REFERENCE AUTHORS	REFERENCE AUTHORS

5 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Osato, N., Saito, R., Suzuki, H., Yamana, A., Miyasaka, H., Yaagi, K., Tomaru, Y., Haegawa, Y., Nogami, A., Kitayama, C., Gotojori, T., Baldarelli, R., Hill, D. P., Bulc, C., Schonbach, C., Quackenbush, J., Schriml, L. M., Kanpin, A., Matsuda, H., Hume, D. A., Quackenbush, J., Shkriyl, L. M., Kanpin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corpani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gatiboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guticinski, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. Z., Konagaya, A., Kurouchkin, I. V., Lee, Y., Lemhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pettes, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tonit, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Waterman, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirokawa-Kishikawa, T., Komuro, H., Nakamura, Y., Sakazume, N., Satoh, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

PANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

1246851

6 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Fritsch, M. C., Medina, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Zhao, M., Davis, M., Wilmong, L. G., Aldrich, S., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Attalaya, R. N., Bailey, T. L., Banerji, M., Baxter, L., Beisel, K. W., Bersano, T., Bonio, H., Chalk, A. M., Chow, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Chu, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Heminger, P., Gingeras, T. R., Gotojori, T., Green, R. E., Guticinski, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Humnickel, L., Iacono, M., Ikeo, K., Iwama, A., Isikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keles, J., Kitanura, H., Kitano, H., Kollias, G., Krishnan, S. P., Kruger, A., Kumarfeld, S. K., Kutuchkin, I. V., Lareau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Lin, S., McWilliam, S., Madan Babu, M., Mader, M., Marchionni, L., Matsuda, H., Matsumura, S., Miki, H., Misgione, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. P., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C. A., Seno, S., Seese, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S. L., Tang, S., Taylor, M. S., Tegener, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yaagi, K., Yamashita, H., Zaborovskiy, E., Zhu, S., Zimmer, A., Hilde, M., Bulc, C., Grimond, S. M., Teasdale, R. D., Liu, E. T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imanura, K., Itoh, M., Kato, T., Kawasaki, H., Kawagashira, N., Kawashima, T., Koike, M., Kondo, S., Konno, H., Nakano, K., Niimura, N., Nishio, T., Okada, M., Plesey, A., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okumura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.

The transcriptional landscape of the mammalian genome

PANTOM Consortium

JOURNAL	Science 309 (5740), 1559-1563 (2005)
PUBMED	16141072
REFERENCE	
AUTHORS	7 Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yip, C.-C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Fritch, M., Ravasi, T., Pang, K. C., Hallinan, J., Mattick, J., Hume, D. A., Lipovich, L., Batalov, S., Engstrom, P. G., Mizuno, Y., Feghthi, M. A., Sandelin, A., Chalk, A. M., Mottagui-Tabar, S., Liang, Z., Lennard, B. and Wallested, C.
CONSRMT	RIKEN Genome Exploration Research Group
TITLE	Antisense transcription in the mammalian transcriptome
JOURNAL	Science 309 (5740), 1564-1566 (2005)
PUBMED	16141073
REFERENCE	
AUTHORS	8 (bases 1 to 1769) Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Horii, F., Iida, J., Imanura, K., Imocani, K., Itoh, M., Kanagawa, S., Kawai, J., Koijima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wataniki, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ , Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ .
FEATURES	Location/Qualifiers
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CDS	
ORIGIN	
Alignment Scores:	
Pred. No.:	0.804 Length: 1769
Score:	107.00 Matches: 49
Percent Similarity:	40.2% Conservative: 31
Best Local Similarity:	24.6% Mismatches: 65
Query Match:	8.7% Indels: 54
DB:	Gaps: 11

US-10-817-483-2 (1-239) x AKI66259 (1-1769)

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Oy      55  GlyThrThrArgLeuTyLeuAspArgProLeuValLysGlyIleIleThrAlaLys 74
Db      318  GGC-----GGCGTGTGTCCCGGCG 338
Oy      75  GlnAlaHisGluArgLeuIleAlaGluValHisAsnHis-----GluAlaLys 90
Db      339  GACTACACCCAGCTGATGATGATTTCCACCAAGGCGGAGCGACGACGCCGCTCGAGGCGCAAG 398
Oy      91  GlyIleuLeuIleuGluGlyGlySerIleSerIleuArgCysMetAlaGlnSerArg 110
Db      399  GCTGGGGTGGCGCTGAGC-----TCCCTGCTGGCGCTC-----431
Oy      111  TyrTrpAsnAlaAspPheArgTrpHisIleIleArgAsn---GluLeuAlaAspGluGlu 129
Db      432  -----GCCAAGTTCGAGGCCACGAGGCTGTAACTTCACTTGCTGAGCGAAGAG 482
Oy      130  SerPheMetSerValAlaIleThrArgValLysGlnMetLeuArgProSerAlaGlyLeu 149
Db      483  GCCAGCGCGGAGGAGGCGCAAGGCCCTGCTGGGAGGCTCTGCGCCGCCGCGCGGCTTC 542
Oy      150  Ser-----IleIleGlnIleuValGlnIleuTrpArgGluProArgLeuArgPro 166
Db      543  AAGTGCAAGGCAATCTTCCATGATGATGCTGCTGTGCTG-----ACAGATAGAGCTTCCCC 596
Oy      167  IleuGluGlyIleAspGlyTyArgTyAla-----177
Db      597  GTCCGAGGAGGCGCCAGCAAGACTTCCAGTCTGCTGCGGAGCCTACACGACGACTCC 656
Oy      178  -----LeuIleuPheAlaThrGlnAsnGlnIleThrPro-----AspMetLeuLeu 192
Db      657  ATCTTCTTCTCTCTCCGCTTGCATGACACCAATCATATGCCAAAGAGATCCCGAGATCATC 716
Oy      193  GlnIleuAspAlaAspMetGluAsnLysLeu---IleHisGlyIleAlaGlnGluPhe 210
Db      717  CAGCTGGACCTTGACCTGAAGTATATAGACCAACAATCCGAGAGCTGTTGAGGAGATTTC 773

RESULT 8
CC3911172/c      831 bp      DNA      linear      GSS 19-MAY-2007
LOCUS      PUHCY57TD ZM.0.6.1.0 KB Zea mays genomic clone ZMMB7423117,
DEFINITION      genomic survey sequence.
ACCESSION      CC3911172
VERSION      CC3911172.1 GI:30871262
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 831)
WhiteLau,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Reinick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Benneken,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUHCY57TB
Contact: Cathy WhiteLau
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteLau@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..831
/organism="Zea mays"
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Db 850 AGGTGCTTCTGATTGTTGGCTTGCGCTCGCATTTAGAAAAGTTTGG 897

RESULT 10
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DEFINITION CGA123-E10.y1d-s SHGC-CGX2 Gasterosteus aculeatus cDNA clone
ACCESSION DMS96236
VERSION DMS96236.1 GI:85172170
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
REFERENCE 1 (bases 1 to 1113)
Kingsley,D.M., Peichel,C., Knecht,A., Balabhadra,S., Grimwood,J.,
Dickson,M., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus (2004)
JOURNAL Unpublished (2004)
COMMENT Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@hgc.stanford.edu
Plate: 123
High quality sequence stop: 889.
Location/Qualifiers
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/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
/clone="CGA123-E10"
/sex="mixed male and female"
/tissue_type="eyes"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CGX2"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTGATTCGATCGACGCGCGCC(7)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa9.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0.612	105.50	41.5%	22.7%	8.6%	1113	47	39	84	37	11

US-10-817-483-2 (1-239) * DMS96236 (1-1113)

QY 33 AsparagVAlGInGcYsCysProGInLeuserThrGlySerGlyArgProThrValGluGlu 52
Db 197 GACCGCTTCTCGCATTTATGCTTGCGCTTGCGATCCAGACGCTTTGGGGAGAG 256
QY 53 LeuYsGlyThrThrArgLeuTyTrpLeuAspA-----ArgProLeuValYsGlyLe 70
Db 257 TTATACAGAGAGACCAAGAGCTTTCTTGAGAAATCATGTCGCAATTATACAGAAAGTC 316
QY 71 lIethrAlaYsGlnAlaHIsGlnArgLeuIleAlaGluValHIsAsnHIs-----Glu 88
Db 317 CTA-----GAATCAGAGAGAAAGTTTAGATGATGATACACAGATACGCGAG 367
QY 89 AlaYsGlyGlyLeuIleLeuGlnGlySerIleSerIleLeuArgCysMetAlaGln 108
Db 368 TACAGCAGAGGA-----GCTGACTCATGAGACTGCTTG----- 400
QY 109 SerArgTyTrpAsnAlaAspPheArgTrpHisIleIleArgAsnGluLeuAlaAspGlu 128
Db 401 TACAGGATTCACACATCAGTTC-----ATCAGAGAGACAACTACAGAGACA 451
QY 129 GluSerPheMetSerValAlaYsThrArgValYsGlnMetLeuArgProSerAlaGly 148
Db 452 GACCTGCAGTACGGCTACGATGCGGGGTGACATGAACGAGCCGCTC----- 496
QY 149 LeuserIleIleGlnGlnLeuValGlnLeuTrpArgGluProArgLeuArgProIleLeu 168
Db 497 ATGAGATCGAGAGAGCTGCGCTCGACATGTGGAGAGAACTAATGATGAGCCCTTCAG 556
QY 169 GluGlyIleAspGlyTyTrArgTyAlaLeuLeuPheAlaThrGlnAsnGlnIleThrPro 188
Db 557 GAT-----GTCCTGATCCGAGATGCTGTAATGAATCAAAAT 595
QY 189 AspMetLeuGlnLeuAspAlaAspMetGlnAsnYsLeuIleHIsGlyIleAlaGln 208
Db 596 GAC-----CGTTGGGAGAGAACCTTAACAGAGAGTCATCCAGGGGTCAATCAAC 646
QY 209 GluPheLeuIleHIsAlaArgArgGlnGlnGlnIlePheProLeuValGlyAlaThrAla 228
Db 647 TCCTTT---GTTCATGTTGAACAGTACAGAAAGATTTCCATC-----AAGTTTAT 697
QY 229 ValGluAlaPheGlnGlyPro 235
Db 698 CAGGAATCTTCAGAGGAGCA 718

RESULT 11
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DEFINITION JGI_ANNO47121.fwd ANNO Pimephales promelas whole (M) Pimephales
LOCUS DT179124
ACCESSION DT179124.1 GI:73439175
VERSION DT179124.1
KEYWORDS EST.
SOURCE Pimephales promelas
ORGANISM Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Pimephales.
REFERENCE 1 (bases 1 to 876)
Richardson,P., Lucas,S., Rokhsar,D., Deter,J.C., Ng,D.C.,
Broksstein,P. and Lindquist,E.A.
DOE Joint Genome Institute Pimephales promelas EST project
JOURNAL Unpublished (2005)
COMMENT Other ESTs: JGI_ANNO47121.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
CDNA Library Preparation: DOE Joint Genome Institute:
<http://www.jgi.doe.gov>
DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
Naming Conventions: EST name is generated by the concatenation of

JOURNAL COMMENT
Unpublished (2005)
Other_ESTS: JGI_CAAV2005.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
CDNA library preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix ' fwd', indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CAAV 0021 row: 1 column: 21
High quality sequence stop: 860.
Location/Qualifiers

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/db_xref="taxon:90988"
/clone="CAV2005"
/tissue_type="testis"
/clone_lib="CAV Pimephales promelas testis 7-8 month adults, males and females pooled (H)"
/notes="Vector: pCMVSPORT6; The library was made from dt primed cDNA and cloned into Invitrogen vector pCMVSPORT6. Poly A RNA were primed with an oligo dt primer (5'-GACTAGTTCTGATCGGAGCGGCGCCCTTTTCTTTT-3') ligated to a SalI adapter (5'-TCGACCCAGCGGTCCG and 5'-CGACGCGGTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L ~0.5-1.2k, M ~1.2-2.5k, H ~>2.5k) then ligated into NotI and SalI digested pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute."

ORIGIN

Alignment Scores:

Pred. No.: 0.966 Length: 881
Score: 102.50 Matches: 51
Percent Similarity: 38.4% Conservative: 27
Best Local Similarity: 25.1% Mismatches: 72
Query Match: 8.3% Indels: 53
DB: 10 Gaps: 10

US-10-817-483-2 (1-239) x DT267881 (1-881)

QY 37 CysCysProGlnLeuSerThrGlySerGlyValPro-----ThrValGln 51
Db 206 TGCTGC-----TCTTTGGGGCAGGGGAGATCTTCTCGAACTCCGTGTCAATTGAG 256
QY 52 GluLeuIysGlyThrThrArgLeuTyrlleuAspAspArgProLeuValIlelle 71
Db 257 GAAGTCAAGGCTCTTGTGCTC-----TCTATTCTC 289
QY 72 ThrAlaIysGlnAlaHis-----GluArgLeuIleAlaGluValHisAsnHisGlu 88
Db 290 ATGGGCGCTTCAAGGCCACGTTGAGCCAGAGATGTACTGTCTCGGACCATCACCATTGCG 349
QY 89 AlaIysGlyGlyLeuIleGluGlyGlySerIleSerLeuLeuArgCysMetAlaGln 108
Db 350 CGCATGGCTCCAGAAATGTGTAG-----CTCTTTACAGACCATGTCACTC 397
QY 109 SerArgTyrrTpaAsnAlaAspPheArgTrpHisIle-----120
Db 398 AAAGCGCTTC-----AAGCAGATCAGAGACTCACATCCGAATGAGAGCATGCTGTGAG 451
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPhe-----MetSerValAlaIys 136
Db 452 AACGAAACCAAGATGTGACAGAGTGTCTTTTTCAGCCGATGTCAGATCCTGTGCTG 511
QY 137 ThrArgValIysGlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuVal 156

Db 512 ACAAGCATGGCGGAGGCGCTACAGGCCAAACAGTGTCTGACATCGATCAAGCTTTTCTA 571
QY 157 GlnLeuTrp-----ArgGlnProArgLeuArg 165
Db 572 CCCAGCATGACAAAGAAATGCTCAGAGAGAGTAGAAATTCACAGCCAGAGATATG 631
QY 166 ProIleuGluGlyIleAspGlyTyrrArgTyrrAlaLeuPheAlaThrGlnAsnGln 185
Db 632 CTACTGTGTACTCAAGTACAGCTACTGCTTAACCTGTTTAACTCAAGAG 691
QY 186 IleThrProAspMet-----LeuLeuGlnLeuAspAlaAspMetGluAsnIys 201
Db 692 AAAAACAAGACTTGGAGAAATTTAGTTTACTCACTGATGATGAGGCTTTGAGAGTAA 751
QY 202 LeuIleHis 204
Db 752 CATCATCAC 760

RESULT 15
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LOCUS
DEFINITION
IMAGE:7193158 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murine; Rattus.
1 (bases 1 to 818)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
NHLBI National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabds-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLNL at:
http://image.llnl.gov
Plate: LLM15054 row: p column: 20
High quality sequence stop: 622.
Location/Qualifiers

FEATURES
source

1..818
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/db_xref="taxon:10116"
/clone="IMAGE:7193158"
/tissue_type="heart, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_234"
/note="Organ: heart; Vector: pExpress-1; Site 1: SCORV; Site 2: NotI; RNA obtained from pooled heart tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTGATCGGAGCGGCGCCCTT-3' and cloned into the SCORV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_233) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 19:47:30 ; Search time 187 Seconds
(without alignments)
3587.126 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1230	100.0	5622	4	US-09-545-334B-7
5	1005	81.7	723	3	US-09-434-837-12
6	1005	81.7	745	3	US-09-073-587-4
7	1005	81.7	24595	10	5428147-1
8	995	80.9	3182	3	US-08-971-395-1

9	994	80.8	747	3	US-09-434-837-5	Sequence 5, Appl1
10	984	80.0	3183	2	US-08-413-135-1	Sequence 1, Appl1
11	686.5	55.8	2544	3	US-09-434-837-9	Sequence 9, Appl1
12	557	45.3	584	2	US-08-054-985-2	Sequence 2, Appl1
13	122.5	10.0	897	3	US-09-902-540-3420	Sequence 3420, Ap
14	122.5	10.0	18192	3	US-09-902-540-1162	Sequence 1162, Ap
15	110	8.9	1026	3	US-09-602-787A-277	Sequence 277, Ap
16	106	8.6	951	3	US-09-328-352-2809	Sequence 2809, Ap
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18	103.5	8.4	4415292	3	US-09-103-840A-1	Sequence 1, Appl1
19	101	8.2	990	3	US-09-710-279-1459	Sequence 1459, Ap
20	101	8.2	3775	3	US-09-710-279-3882	Sequence 3882, Ap
21	100	8.1	1830121	3	US-09-557-884-1	Sequence 1, Appl1
22	100	8.1	1830121	3	US-09-643-990A-1	Sequence 1, Appl1
23	100	8.1	1830121	3	US-10-158-865-1	Sequence 1, Appl1
24	98.5	8.0	1119	3	US-09-540-236-1701	Sequence 1701, Ap
25	97.5	7.9	945	3	US-09-543-681A-1567	Sequence 1567, Ap
26	96.5	7.8	3482	4	US-10-094-748-643	Sequence 643, Ap
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28	95.5	7.8	1866	3	US-08-909-742-1	Sequence 1, Appl1
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35	91	7.4	70559	3	US-09-409-800B-1	Sequence 1, Appl1
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37	88	7.2	846	3	US-08-936-165A-65	Sequence 65, Appl
38	88	7.2	1701	3	US-09-902-540-5141	Sequence 5141, Ap
39	88	7.2	1884	3	US-09-902-540-4066	Sequence 4066, Ap
40	88	7.2	2041	3	US-09-513-151A-3	Sequence 3, Appl1
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42	88	7.2	11854	3	US-09-902-540-1037	Sequence 1037, Ap
43	88	7.2	21511	3	US-09-902-540-1301	Sequence 1201, Ap
44	87.5	7.1	5884	3	US-09-221-017B-497	Sequence 497, Ap
45	87	7.1	14823	3	US-09-902-540-1087	Sequence 1087, Ap

ALIGNMENTS

RESULT 1
US-09-545-334B-8
; Sequence 8, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Haben, Jeff
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; TITLE OF INVENTION: Seeds
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Hordeum vulgare, Plant Journal 6:849-860
; OTHER INFORMATION: (1994): gene from Agrobacterium tumefaciens, Molecular
; OTHER INFORMATION: and General Genetics 216:388-394 (1989): terminator
; OTHER INFORMATION: from Zea mays, Gendank Accession #S78780.
US-09-545-334B-8
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Pred. No.: 1.11e-138 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0

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Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
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RESULT 2
US-09-545-334B-9
; Sequence 9, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2722
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TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648;
; OTHER INFORMATION: gene from Agrobacterium tumefaciens, Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989); terminator from Solanum
; OTHER INFORMATION: tuberosum, Plant Cell 1(1):115-122 (1989).
US-09-545-334B-9
Alignment Scores:
Pred. No.: 1,11e-138 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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Qy 161 GluProArgLeuArgProIleLeuGluGlyLysAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db GAGCTCGCTGAGAGGCCCATCTGAGAAAGGATCGATGATCGATATGCCCCCTGCTATT 2064
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
Db GCTACCCGAACCGATACAGCCCGCATATGCTATTGCTGACCTCGACGCGATATGAGAA 2124
Qy 201 LysLeuIleHisGlyLysIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
Db AAATTGATTCAAGGATCGCTCAGAGTTTCTTAATCCATGCGCGTCGACAGGAACAGAA 2184
Qy 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGluGlyProProPheArgMet 239
Db TTCCCTTGTGGGGCGACAGCTGTGCAAGCGTTTGAAGCACCATTTTCGATG 2241
RESULT 3
US-09-545-334B-12
; Sequence 12, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
```

APPLICANT: Haben, Jeff
APPLICANT: Tomes, Dwight
TITLE OF INVENTION: Regulated Expression of Genes in Plant
FILE REFERENCE: 0803
CURRENT APPLICATION NUMBER: US/09/545,334B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 3017
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from Zea mays, Genbank Accession #U22344;
OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and
OTHER INFORMATION: General Genetics 216:388-394 (1989); terminator from
US-09-545-334B-12

Alignment Scores:
Pred. No.: 1,3e-138 Length: 3017
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-817-483-2 (1-239) x US-09-545-334B-12 (1-3017)

Qy 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleala 20
Db 1408 ATGATCTACGCTAATTTTCGTCCTCACTGACAGAAAGACATCGATCGATAGCT 1467
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 1468 CTGGCCAGACAGACAGGCTCCAGCTCTGCTCGATCGGCTCAATGCTGCTCTCA 1527
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuThr 60
Db 1528 CTATCAACCGGAAGCGGGGAGCAACAGTGAAGAACTGAAGAAAGCACTGCTGTC 1587
Qy 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 1588 CTGTATGATCGCCTTTGGTAAAGGTATCATTTACAGCAACAGCTCATGACGGCTC 1647
Qy 81 IleAlaGluValHisAsnHisGluAlaLysGlyLysLeuIleLeuGluGlyLysSerIle 100
Db 1648 ATTTGGAGGTGCACAAATCAGAGGCAAGCGGCTTATCTTGAAGGAGATCTATC 1707
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 1708 TCGTTGCTCAGGTGATGGCCGAAGCTCTTATTTGAAGCGCGATTTTCGTCATATT 1767
Qy 121 IleArgAsnGluLeuAlaAspGluLysPheMetSerValAlaLysThrArgValLys 140
Db 1768 ATTGCAACGAGTTTACAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGAGTTAAG 1827
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 1828 CAGATGTTACGCCCTCTGCAAGCTTTCTATTATTCACAGAGTTGGTTCACTTTGAGG 1887
Qy 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 1888 GAGCTCGGCTGAGGCGCATCTGGAAGGATCGATGATATCGATATGCTCTGCTATT 1947
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 1948 GCTACCCAGAACCAAGATCAGCGCCGATATGCTATTGAGCTGACAGCAGATATGAGAA 2007
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220

Db 2008 AAATTGATTCACGATATTCCTCAGAGATTTCTAATTCATCCGCGTGCACAGAAAGAA 2067
Qy 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 2068 TTCCTTTGTTGGTGGCGGACAGCTGTGGAAGGCTTTGAAGGACCAACCATTTGGAATG 2124

RESULT 4
US-09-545-334B-7
Sequence 7, Application US/09545334B
Patent No. 6992237

GENERAL INFORMATION:
APPLICANT: Zinselmeier, Chris
APPLICANT: Haben, Jeff
APPLICANT: Tomes, Dwight
TITLE OF INVENTION: Regulated Expression of Genes in Plant
FILE REFERENCE: 0803
CURRENT APPLICATION NUMBER: US/09/545,334B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 5622
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter and terminator from Zea mays as found in
OTHER INFORMATION: Genbank Accession #S78780; gene from Agrobacterium
OTHER INFORMATION: tumefaciens as found in Molecular and General
US-09-545-334B-7

Alignment Scores:
Pred. No.: 3,3e-138 Length: 5622
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-817-483-2 (1-239) x US-09-545-334B-7 (1-5622)

Qy 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleala 20
Db 1525 ATGATCTACGCTAATTTTCGTCCTCACTGACAGAAAGACATCGATCGATAGCT 1584
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 1585 CTGGCCAGACAGACAGGCTCCAGCTCTGCTCGATCGGCTCAATGCTGCTCTCA 1644
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuThr 60
Db 1645 CTATCAACCGGAAGCGGAGCAACAGTGAAGAACTGAAGAAAGCACTGCTCTGAC 1704
Qy 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 1705 CTGTATGATCGCCTTTGGTAAAGGTATCATTTACAGCAACAGCTCATGACGGCTC 1764
Qy 81 IleAlaGluValHisAsnHisGluAlaLysGlyLysLeuIleLeuGluGlyLysSerIle 100
Db 1765 ATTGCGAGGTGCACAAATCAGAGGCAAGCGGCTTATCTTGAAGGAGATCTATC 1824
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 1825 TCGTTGCTCAGGTGATGGCCGAAGCTCTTATTTGAAGCGCGATTTTCGTTGGCATATT 1884
Qy 121 IleArgAsnGluLeuAlaAspGluLysPheMetSerValAlaLysThrArgValLys 140
Db 1885 ATTCGCAACGAGTTTACAGAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGATTAAG 1944

QY 141 GIMMELUARGPROSERALAGLYLEUSERILEIIEGNGULUENVALGINLEUTPRAG 160
DB 1945 CAGATGTTACGCCCTTCGCGAGGCTTCTATATTCAGAGGTTGTTCACTTGAGAGG 2004
QY 161 GIUPTROARGLEUARGPROILEUENGLIYLEASPGLYTYRARGTYRALALEUENPHE 180
DB 2005 GAGCTCGGCTGAGGCCCATCTGMAAGGATCGATGATTCATATGATCCCTCTATT 2064
QY 181 ALATHRGLNANGINILETHPRASPMECLEUENGLUENASPAALASPMECGLUASN 200
DB 2065 GCTACCCAGAACAGATACAGCCCGATATGCTATTGACGCTGACGACGATATGAGAA 2124
QY 201 LYSLEULEHISGLYILEALINGLUPHEULEULEHISALAAARGAGLNGULNYS 220
DB 2125 AAATGTATTCACGGTATCGCTCAGAGATTCTAATCCATGCGCGTCGACAGAA 2184
QY 221 PHEPROLEUVALGIALATHRALAVAGLUALAPHEGLUGLYPROPROPHEARGMET 239
DB 2185 TTCCCTTTGGTGGCGGACAGCTGTGCAACGTTTGAAAGACCACTTCGAA 2241

RESULT 5

US-09-434-837-12
Sequence 12, Application US/09434837
Patent No. 6756574
GENERAL INFORMATION:
APPLICANT: Ream, Walt et al.,
TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
FILE REFERENCE: 53629
CURRENT APPLICATION NUMBER: US/09/434,837
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: 60/107,185
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 723
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-09-434-837-12

Alignment Scores:

Pred. No.: 2.97e-112 Length: 723
Score: 1005.00 Matches: 193
Percent Similarity: 88.7% Conservative: 19
Best Local Similarity: 80.8% Mismatches: 27
Query Match: 81.7% Indels: 0
Gaps: 0

US-10-817-483-2 (1-239) * US-09-434-837-12 (1-723)

QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGGACCTGCATCTAATTTTGGTTCACACTTGACAGAGAAAGACAGACCGCGATCT 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTGGCCGACAGACGAGGCTTCACATCTTCGCTTGATCGGCTCCAAATGCTGCTCTAA 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 121 CTATCAACCGAAGGAGGACGACCAACATGGAGAACTGAAAGCAACAGCGGCTTCTAC 180
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnuArgLeu 80
DB 181 CTTGATGATCGGCTCTGTTGAGGATATCATCGACGCAAGCTCATATGAGCTG 240
QY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyIleLeuGlnGlyIleGlySerIle 100
DB 241 ATCGAGGAGGTGTATTAATCATGAGGCAACGCGGCTTATCTTGAAGGAGATCCACC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120

DB 301 TCGTGTCTCAACTGCATGAGCGCGAAGACGCTATTGAGTGCAGATTTTCGTTGCATATT 360
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 361 ATTGCGCAACAAGTATACCGGACCAAGAGACCTCTCTGAAAGCGGCAAGGCGCAAGTAA 420
QY 141 GIMMELUARGPROSERALAGLYLEUSERILEIIEGNGULUENVALGINLEUTPRAG 160
DB 421 CAGATGTTGACCCCGCGAGGCCCATCTTCTATATTCAGAGGTTGTTCACTTGAGAGG 480
QY 161 GIUPTROARGLEUARGPROILEUENGLIYLEASPGLYTYRARGTYRALALEUENPHE 180
DB 481 GAACCTCGGCTGAGGCCCATTTCTAAGAGATGATGATGATATGATATGATGATGATG 540
QY 181 ALATHRGLNANGINILETHPRASPMECLEUENGLUENASPAALASPMECGLUASN 200
DB 541 GCTAGCCAGAACAGATACAGCGCAGATATGCTATTGACGCTTGCAGAAATATGAAAGT 600
QY 201 LYSLEULEHISGLYILEALINGLUPHEULEULEHISALAAARGAGLNGULNYS 220
DB 601 AAGTTGATTAATGGATCGCTCAGAGATTTCTAATCCATGCGCGCAACAGAAACAGAA 660
QY 221 PHEPROLEUVALGIALATHRALAVAGLUALAPHEGLUGLYPROPROPHEARGMET 239
DB 661 TTCCCCCAAGTTACGACGCGCTTTCGACGATTCGAAGTCAATCCGTTGGAATG 717

RESULT 6

US-09-073-587-4
Sequence 4, Application US/09073587
Patent No. 6268552

GENERAL INFORMATION:
APPLICANT: Li, Yi
TITLE OF INVENTION: Transgenic Seedless Plants
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,587
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,725
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..725
US-09-073-587-4

Alignment Scores:

Pred. No.: 3,1e-112 Length: 745
 Score: 1005.00 Matches: 193
 Percent Similarity: 88.7% Conservative: 19
 Best Local Similarity: 80.8% Mismatches: 27
 Query Match: 81.7% Indels: 0
 DB: 3 Gaps: 0

US-10-817-483-2 (1-239) x US-09-073-587-4 (1-745)

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Oy 1 MetaspleuAargyleuilePhegilyProthrcystrhgilyvsthrSerThralaileala 20
Db 3 ATGGACCTGCATCTAATTTTCGCTCCAACTTCACAGGAAACGACGACCGCGATAGCT 62
Oy 21 LeuAlagInglInThrglyLeuProValleuSerleuAsparValGlnCysCysProGln 40
Db 63 CTGGCCAGACAGAGGGGCTTCAGTCCCTTCCTTGATCGGGTCCAAATGCTGCTCA 122
Oy 41 LeuSerThrglySerGlyAargProThrValGluGluLeuLysGlyThrThraArgLeuTy 60
Db 123 CTATCAACCGGAGGAGGACGACCAACAGTGAAGAACTGAAGAAAGACGACGCTCTAC 182
Oy 61 LeuAsparAargProleuVallysglyleileThralalyglnAlahisgluArgleu 80
Db 183 CTTGATGATCGGCTCTGCTGGAGGGATATCATCGACGACCAAGCTCATATAGGCTG 242
Oy 81 lLealagluValhIsasnhisgluAlalysglyLeuileLeuGluGlyGlySerile 100
Db 243 ATCGAGGAGGTATATATCATATGAGGCCAAGCGGGCTTATCTTGAGGAGATCCACC 302
Oy 101 SerleuLeuAargCysMetAlagInserArgTyrrTPasnaAlaaspPheArgTrpHisile 120
Db 303 TCGTGTCTCAACTGCATGCGCGGAAACAGCTATTCAGAGTCAGATTTTCGTTGCGATATT 362
Oy 121 lLeaArgangluLeuAlaaspGluLuserPheMetSerValAlalyThraArgVallys 140
Db 363 ATTCGCCCAAGATTACCGGACCAAGACCTTCATGAAGAACCGGCCCAAGGCTTAAAG 422
Oy 141 GlnMetLeuAargProSerAlaglyLeuSerileileGlnGluLeuValGlnleuTrpArg 160
Db 423 CAGATGTTGCAACCCGCGTGCAGGCGCATTTATTCATCAAGATTCGTTATTTGGAAAT 482
Oy 161 GluProAargLeuAargProileuGluGlylleaspGlyTyrrArgTyrrAlaleuLeuPhe 180
Db 483 GAACCTCGCTGAGGCGCCATTCGAAAGAGATCGATGATATCGATATGCCATGTTGTTT 542
Oy 181 AlaThrgInaengInleThrProaspMetLeuGlnleuAspAlaaspMetGluasn 200
Db 543 GCTAGCCCAAGATCAAGATCAAGGATATGCTATTGTCAGCTTGACGCAAAATATGGAAGT 602
Oy 201 LysleuilehIsglyllealagIngluPheleuilehIsalAargArgGlnGluInlys 220
Db 603 AAGTTGATTAATGGATGCTCTCAGAGATATTCATCCATGCCGCGCAACAGAAACAGAAA 662
Oy 221 PheProleuValGlyAlaThralaValGluAlaPheGluGlyProProPheArgMet 239
Db 663 TTCCCGCCCAAGTTAAGCAGCGCGCTTCGACGATTCGAAGGTCATCGCTCGAATG 719

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RESULT 7

5428147-1

Patent No. 5428147
 APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
 TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
 NUMBER OF SEQUENCES: 17
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/91,538
 FILING DATE: 13-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 869,216
 FILING DATE: 13-APR-1992
 APPLICATION NUMBER: 869,216
 FILING DATE: 13-APR-1992

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; APPLICATION NUMBER: 440,432
; FILING DATE: 21-NOV-1989
; APPLICATION NUMBER: 553,786
; FILING DATE: 19-NOV-1983
; APPLICATION NUMBER: 741,034
; FILING DATE: 06-AUG-1991
; APPLICATION NUMBER: 144,775
; FILING DATE: 20-JAN-1988
; APPLICATION NUMBER: 485,614
; FILING DATE: 15-APR-1983
; APPLICATION NUMBER: 713,624
; FILING DATE: 10-JUN-1991
; APPLICATION NUMBER: 260,574
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: 848,733
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 535,354
; FILING DATE: 26-SEP-1983
; SEQ ID NO:1:
; LENGTH: 24595
; 5428147-1

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Alignment Scores:

Pred. No.: 5,81e-110 Length: 24595
 Score: 1005.00 Matches: 193
 Percent Similarity: 88.7% Conservative: 19
 Best Local Similarity: 80.8% Mismatches: 27
 Query Match: 81.7% Indels: 0
 DB: 10 Gaps: 0

US-10-817-483-2 (1-239) x 5428147-1 (1-24595)

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Oy 1 MetaspleuAargyleuilePhegilyProthrcystrhgilyvsthrSerThralaileala 20
Db 8771 ATGACCTGCATCTAATTTTCGCTCCAACTTCACAGGAAACGACGACCGCGATAGCT 8830
Oy 21 LeuAlagInglInThrglyLeuProValleuSerleuAsparValGlnCysCysProGln 40
Db 8831 CTGGCCAGACAGAGGGGCTTCAGTCCCTTCCTTGATCGGGTCCAAATGCTGCTCA 8890
Oy 41 LeuSerThrglySerGlyAargProThrValGluGluLeuLysGlyThrThraArgLeuTy 60
Db 8891 CTATCAACCGGAGGAGGACGACCAACAGTGAAGAACTGAAGAAACGACGCTCTTAC 8950
Oy 61 LeuAsparAargProleuVallysglyleileThralalyglnAlahisgluArgleu 80
Db 8951 CTTGATGATCGGCTCTGCTGGAGGGTATCATCGACGCAAGCTCATATAGGCTG 9010
Oy 81 lLealagluValhIsasnhisgluAlalysglyLeuileLeuGluGlyGlySerile 100
Db 9011 ATCGAGGAGGTATATCATATGAGGCCAAGCGGGCTTATCTTGAGGAGATCCACC 9070
Oy 101 SerleuLeuAargCysMetAlagInserArgTyrrTPasnaAlaaspPheArgTrpHisile 120
Db 9071 TCGTGTCTCAACTGCATGCGCGGAAACAGCTATTCGAGAGATTTTCGTTGCGATATT 9130
Oy 121 lLeaArgangluLeuAlaaspGluLuserPheMetSerValAlalyThraArgVallys 140
Db 9131 ATTCGCCCAAGATTACCGGACCAAGACCTTCATGAAGAACCGGCCCAAGGCTTAAAG 9190
Oy 141 GlnMetLeuAargProSerAlaglyLeuSerileileGlnGluLeuValGlnleuTrpArg 160
Db 9191 CAGATGTTGCAACCCGCGTGCAGGCGCATTTATTCATCAAGATTCGTTATTTGGAAAT 9250
Oy 161 GluProAargLeuAargProileuGluGlylleaspGlyTyrrArgTyrrAlaleuLeuPhe 180
Db 9251 GAACCTCGCTGAGGCGCCATTCGAAAGAGATCGATGATATCGATATGCCATGTTGTTT 9310
Oy 181 AlaThrgInaengInleThrProaspMetLeuGlnleuAspAlaaspMetGluasn 200
Db 9311 GCTAGCCCAAGATCAAGATCAAGGATATGCTATTGTCAGCTTGACGCAAAATATGGAAGT 9370
Oy 201 LysleuilehIsglyllealagIngluPheleuilehIsalAargArgGlnGluInlys 220

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Db 9371 AAGTTGATTATATGGATCGCTCAGAGATTTTCATCCATGCGCCCAACAGAAACAGAA 9430
Qy 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 9431 TTCCCCAAGATTACGACGCGCTTTCGACCGATTCCAGAGTCATCCGTTCCGATG 9487

RESULT 8
US-08-971-395-1
; Sequence 1, Application US/08971395
; Patent No. 6359197
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; APPLICANT: No. 6359197, Yoo-Sun
; APPLICANT: Gan, Susheng
; TITLE OF INVENTION: Transgenic plants with altered
; TITLE OF INVENTION: Senescence Characteristics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,395
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.94908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-971-395-1

Alignment Scores:
Pred. No.: 4,45e-110 Length: 3182
Score: 995.00 Matches: 192
Percent Similarity: 88.3% Conservative: 19
Best Local Similarity: 80.3% Mismatches: 28
Query Match: 80.9% Indels: 0
Gaps: 0
DB: 3

US-10-817-483-2 (1-239) x US-08-971-395-1 (1-3182)
Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db 2181 ATGGAACCTGCAATCTTAATTTGGGTCCAACTTGACAGGAAAGACGACGCGCATAGCT 2240
Qy 21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
Db 2241 CTTGCCACGACGACGAGGCTTCAGTCTTCGCTGATCGGCTCAATCGTCTCAAA 2300
Qy 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuThr 60
Db 2301 CTATCAACCGGAGACGAGACCAACAGTGGAAAGAACTGAAAGAACGACGCTCTTAC 2360
Qy 61 LeuAspAspArgProLeuValIleGlyIleIleThrAlaLysGlnAlaIleGluArgLeu 80
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Db 2361 CTTGATATATGCGCTTCGTGGAGGATATCATCCAGCCAGCAAGCTCATATAGCTG 2420
Qy 81 IleAlaGluValHisAsnHisGluAlaIleGlyGlyLeuIleLeuGluGlySerIle 100
Db 2421 ATCGAGAGGGGTATATATCATATGAGCCCAAGCGCGGCTTATTTCTTGAGGGAGATCCACC 2480
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 2481 TCGTTGCTCAATCGCAATCGCGCGCAAGACGCTATTGGAGTGAGATTTTCGTGGCATATT 2540
Qy 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db 2541 ATTGCCACCAAGTATCCCGACCAAGACACTTCTATGAAAGGGCCCAAGCCAGAGTTAAG 2600
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 2601 CAGATGTTGACCCCGCTGGAGGCGCATTTCTATTTCAGAAGTTGTTTATCTTTGCAAT 2660
Qy 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuPhe 180
Db 2661 GAACCTCGCTGAGGCCCATTTGTAAAGAGATCATGATATGATATGCCATGTGTTT 2720
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
Db 2721 GCTAGCCAGAACCAAGATCACGCGCATATGCTATTCAGCTTGACCGCAATATGGAAGCT 2780
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
Db 2781 AAGTTGATTATATGAGATCGCTCAGAGATATTTTCATCATGCGGCCCAACAGAAACAGAA 2840
Qy 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 2841 TTCCCCAAGTTAACGACGCGCTTTCGACGAGTATGAAAGTCAATCCGTTCCGATG 2897

RESULT 9
US-09-434-837-5
; Sequence 5, Application US/09434837
; Patent No. 6759574
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/09/434,837
; EARLIER FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 60/107,185
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-434-837-5

Alignment Scores:
Pred. No.: 6,72e-111 Length: 747
Score: 994.00 Matches: 191
Percent Similarity: 88.6% Conservative: 19
Best Local Similarity: 80.6% Mismatches: 27
Query Match: 80.8% Indels: 0
Gaps: 0
DB: 3

US-10-817-483-2 (1-239) x US-09-434-837-5 (1-747)
Qy 3 LeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAlaLeuAla 22
Db 18 CTGAATCTTAATTTTCGCTCAACTTGACAGGAAAGACGAGACCGGATGCTCTTGCC 77
Qy 23 GlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGlnLeuSer 42
Db 78 CAGACGACAGGCGCTTCAGTCTTTCGCTTATGCGGTCGAATGCTGCTCAATATCA 137
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```

: GENERAL INFORMATION:
: APPLICANT: Ream, Walt et al.,
: TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
: FILE REFERENCE: 53629
: CURRENT APPLICATION NUMBER: US/09/434,837
: CURRENT FILING DATE: 1999-11-04
: EARLIER APPLICATION NUMBER: 60/107,185
: EARLIER FILING DATE: 1998-11-05
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 2544
: TYPE: DNA
: ORGANISM: Agrobacterium tumefaciens
: US-09-434-837-9

Alignment Scores:
Pred. No.:      8,23e-73      Length:      2544
Score:          686.50      Matches:      191
Percent Similarity: 25.2%      Conservative: 20
Best Local Similarity: 22.8%      Mismatches: 26
Query Match:      55.8%      Indels:      599
DB:               3      Gaps:      1

US-10-817-483-2 (1-239) x US-09-434-837-9 (1-2544)

QY      3      LeuAArgLeuIlePheGlyProThrCysThrGlyIleThrSerThrAlaIleAlaLeuA1a 22
Db      18      CTGATCATTAATTTTCGGTCCAACTTGCCACAGAAAGACGACCGCATAGCTTCC 77
QY      23      GlnGlnThrGlyLeuProValLeuSerLeuSparGValGlnCysCysProGlnLeuSer 42
Db      78      CAGAGAGAGGGCTTCGACGCTTCCTGATCGGGTCAATGCTGCTCACTATCA 137
QY      43      ThrGlySerGlyAArgProThrValGlnIleuLeuGlyIleThrThrArgLeuTyrLeuAsp 62
Db      138      ACCGGAACCGGACGACCAACAGTGGAAAGACTGAAAGAGACGACCGCTCTACCTTGAT 197
QY      63      AspArgProLeuValIleGlyIleIleThrAlaIleGlnAlaIleGlnArgLeuIleAla 82
Db      198      GATCGGCTCTGTTGGAGGGTATCATCGACCAAGCTCATGAGCTGATCGAG 257
QY      83      GluValHisAsnHisGlnAlaIleGlyIleuIleuGlnIleuGlyIleSerIle----- 100
Db      258      GAGGTATATATCATGAGGCCACGCGGCTTATTTTGAGGAGGATCATGATCATGA 317
QY      100      ----- 100
Db      318      ACCTCTCCTTGATTAACCAAGTCATCTCCCAACCAAAATGTGTGATCTGACATGTGT 377
QY      100      ----- 100
Db      378      CGATTAAGCGGATGAATTGACCGCAGGGTTTCCGATGCTTCTTAGAACGAGAAGCTTC 437
QY      100      ----- 100
Db      438      TAGGGGAAGAGATTACTCAAAAGCTCCACGAGTGACGCGTGGGTTAGCTTGCAAAAG 497
QY      100      ----- 100
Db      498      GCTGGCGGATGTGGCTTCCCGAGATCTCAAGCTGTGTGAAAGGTAGACGTTCTCTCCG 557
QY      100      ----- 100
Db      558      TTATATCTATATTGGCAAAGAATTTCTGGGCGGATACTGTAATCGAAACCTTGGGCGCG 617
QY      100      ----- 100
Db      618      GGCACAGTGAAGTGTCTGTTGCCATGACTTGAGACCAATTGGCATGATTTTCTCCGA 677
QY      100      ----- 100
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Db      678      AGCACTAATATCCAAAGCCCGTTTGTGAGCGGTAAAGATGTGACCGATTGATCT 737
QY      100      ----- 100
Db      738      TAGCATTTGTGTGCGCATTTCAATCTTAAGACTCGCGGTTTCGAAACCTGCCAATGCC 797
QY      100      ----- 100
Db      798      GCTGTACGAAATGGCAGATGAATAATCGTTACCGGGTTTACCATTAACCTTGAAGGGCC 857
QY      100      ----- 100
Db      858      CGTGCATTTGACATGTGTAGCTTATGTGCAAACTGATGCTGAAGGTTCCGACAGTTTC 917
QY      100      ----- 100
Db      918      CTTTCAACAATCGACTTGCTGTCTACGACTGACCGCTTTTGTGACCAATGTCCGATAG 977
QY      100      ----- 100
Db      978      TGGACGATGGGCTTCTTTCCGAGAGATGTTCTTAAGCCGAAAGTGGCGGTCAATTGGCGC 1037
QY      100      ----- 100
Db      1038      TGGCATTTCCGACTCGTGTGTGGCAACGAATGCTTCATGTCTGGGTAGACGATGTTAC 1097
QY      100      ----- 100
Db      1098      AATATATGAAGCAGATGATGCTGTGGAGCAACCTTTGTGATCATGCTTTACAGGACGC 1157
QY      100      ----- 100
Db      1158      TCCTATGTGTGTGGCCGAATGGGGCGGATGCCATTTCTCTGCTGCAATTTCTGTT 1217
QY      100      ----- 100
Db      1218      TTTCTTCGAGGCTTACGGCTGTCTTGATGAGCGGTTCCCAATCCCGACAGT 1277
QY      100      ----- 100
Db      1278      CGACACTTACTGTGCTACCAAGCGTCCAAATACATGTGAAAGCCGGGACGTCGACCC 1337
QY      100      ----- 100
Db      1338      GAACGTGTCATGCGCTTACCAACGAGTTGGCGGTCTTGAAGACGTTTTCATGA 1397
QY      100      ----- 100
Db      1398      GCGATATATTGTGTGGCTTCGCTGTGCTTACTCAGGCTTGAATCAGGACACAT 1457
QY      100      ----- 100
Db      1458      TAGTGGGCTCATGACTCTGGCAAAATTTGGCTGAACCGTTTCGGAGGAGTCTTCTC 1517
QY      100      ----- 100
Db      1518      TTCAGGATAGAGGATCTTTTCTGGCACAACATCTCTGTGTGTAACATGAGTTT 1577
QY      100      ----- 100
Db      1578      CCTCATGATTGGACCTATTCAAGCTAATGGAAATAGATCTGGCGGGTTTGTCCAGT 1637
QY      100      ----- 100
Db      1638      TTTTGAAGCGGGTTTATAGATCTCCGCTGGTGCATCAACGATATGAAAGAAATCA 1697
QY      100      ----- 100
Db      1698      GCGATGTGCCCTGAAGAAATCTGAAATTTCCACGTCCGATCCGATCTGAAGTGTTAA 1757
QY      100      ----- 100
Db      1758      CGGTGTCTGTGAGCGACGCAATATGCAATGTTCAAGTCAGGGCGATTCGAAGAAAA 1817
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QY 100 ----- 100
Db 1818 GACAAAAATAAAGCTTAAGACGGGATATCTGAACCTTTATGATTAAGGTGGT 1877
QY 100 ----- 100
Db 1878 CACATCTGACTCGCAAAATATCCAACTCAGGATGCTCGACATGCGATTAATTTT 1937
QY 100 ----- 100
Db 1938 TCAGGACCAAGTAACCAAGCGTTGATTAACAGCCATATGACAGATCGTCAAACTCTT 1997
QY 100 ----- 100
Db 1998 CCTGATGACTGAACGAAATCTGTGTTAGACATATCTCCGTTCTTGCTCATGGA 2057
QY 101 -----SerleuLeu 103
Db 2058 CCGGATCGCAAAAGCAGTGTATTGCTGACATATGATGTCGACGATCCACTGTTGCTC 2117
QY 104 ATGCTMeTAlaGInSerArgTTrPaenAlaaspPheArgTrpHisIleIleArgAen 123
Db 2118 AACTGATGCGCGAAGAACAGCTATTGAGTGCAGATTTTCGTTGGCATTTATTCGCCAC 2177
QY 124 GtUeuAlaaspGluGluSerPheMetSerValAlaIleYThrArgValIysGlnMetLeu 143
Db 2178 AAGTTACCCGACCAAGAGACCTTCATGAAAGCGCCAAAGCCAGATTAAAGCAGATGTTG 2237
QY 144 ArgProSerAlaGluLeuSerIleIleGlnGluLeuValGlnLeuTrpArgGluProArg 163
Db 2238 CACCCCGCTGACGGCATTCTATATATCAAGAGTGTGTTATCTTTGGAATGAACCTCGG 2297
QY 164 LeuArgProIleLeuGlnGluIleaspGlyTyrArgTyrAlaLeuLeuPheAlaThrGln 183
Db 2298 CTGAGGCCCATCTCTGAAGAGATCGATGATATGCATATGCTATGTTCTGACCCAG 2357
QY 184 AangInIleThrProaspMetLeuLeuGlnLeuaspAlaaspMetGluAsnIle 203
Db 2358 AACCCAGATCACCGCAGATATGCTATGCTAGCTGACGCAAAATATGGAAGTGAATG 2417
QY 204 HisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnIleYsheProLeu 223
Db 2418 AATGGATCTCTCAGAGATATTTCATCCATGCGCGCAACAGAAATATCCCCCAA 2477
QY 224 ValGlyAlaThrAlaValGluAlaPheGluGluIleProPheArgMet 239
Db 2478 GTTAACGACGCGCTTTCGACCGATTCGAAGGTCATCCGTTGGAATG 2525

RESULT 12
US-08-054-985-2
; Sequence 2, Application US/08054985
; Patent No. 5496732
; GENERAL INFORMATION:
; APPLICANT: Smigocki, Ann C
; APPLICANT: Neal Jr, John W
; TITLE OF INVENTION: ENHANCED INSECT RESISTANCE IN PLANTS
; TITLE OF INVENTION: GENETICALLY ENGINEERED WITH A PLANT HORMONE GENE
; TITLE OF INVENTION: INVOLVED
; TITLE OF INVENTION: IN CYTOKININ BIOSYNTHESIS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Room 411, Building 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,985
; FILING DATE: 30-APR-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S
; REGISTRATION NUMBER: 35024
; REFERENCE/DOCKET NUMBER: 0175,92
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 504-6629
; TELEFAX: (301) 504-5060
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium tumefaciens
; US-08-054-985-2

Alignment Scores:
Pred. No.: 4,61e-58 Length: 584
Score: 557.00 Matches: 145
Percent Similarity: 67.7% Conservative: 12
Best Local Similarity: 62.5% Mismatches: 28
Query Match: 45.3% Indels: 49
DB: Gaps: 6

US-10-817-483-2 (1-239) x US-08-054-985-2 (1-584)
QY 1 MetaspLeuArgLeuIlePheGlyProThrCysThrGlyIleThrSerThrAlaIleAla 20
Db 1 ATGGACCTGCATCTATATTTCGTCACAACTTGACAGGAAGACAGACGCGCATAGCT 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArg-ValGlnCysCysProG 40
Db 61 CTGGCCACGACGACGAGG-----CTGGGTCCAATGCTGTCCTCA 99
QY 40 nLeuSerThrGlySerGlyArgProThrValGlnGluLeuIleGlyThrThrArgLeu 60
Db 100 ACTATCAACCGGACGCGACGACCAACAGTGGAGAACTGAAGAAAGACGCGCTCTTA 159
QY 60 rLeuAspAspArgProLeuValIle-GlyIleIleThrAlaIleGlnAlaHisGluArgL 80
Db 160 C-----GGAGGTATCATGCAAGCCAAAGCTCATCATAGGC 198
QY 80 euIleAlaGluValHisAsnHisGlnAlaIleValGly-GlyLeuIleLeuGluGlyIleSer 99
Db 199 TGATCGAGAGAGGTGATATATCATAGAGCCAAAGCGGGCTTA----- 240
QY 100 lIleSerLeuLeuArgCysMetAlaGlnSerArgTyrTrPaenAlaaspPheArgTrpHis 119
Db 241 ---TCGTTGCTCAACTGCATGCGCGGAAAGAGCTATTGGAATGACGATTTTCGTTGGCAT 297
QY 120 lIleIleArgAsnGluLeuAlaaspGluGluSerPheMetSerValAla-IleThrArgVa 139
Db 298 ATTATTGCCACAAAGTTACCGGAC-----GGCCAAAGGCCAAGGT 336
QY 139 lIle-GlnMetLeuArgProSerAlaGlnSerIleIleGlnGluLeuValGlnLeu 159
Db 337 TAAGCCAGATGTGTGACCCCGCTGAGGCCATTCTATTATTA-GAGTTGGTTATCTTT 395
QY 159 rPaArgGluProArgLeuArgProIleLeuGlnGlyIleaspGlyTyrArgTyrAlaLeu 179
Db 396 GGA-----TTTCTGAAGAGATGATGATGATATGATATGATGATG 436
QY 179 eupPheAlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaaspMetG 199
Db 437 TGTTTGTAGCCAGAACGATCAAGCGCATATGCTATTG----- 477
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Db 7617 ATCGGACGGCGAAGCCCTCTCGAGAGGCTGGCTCGGTCCTCATCATCTGCTGCC 7558
Qy 54 ----- 54
Db 7557 GCGGTGAGCCCGATGAGGCGTTCTCCGCTGCTGATACACGCGCGTCCGAGCGCGTC 7498
Qy 55 ----- GlyThrThrArgLeuYr 60
Db 7497 ATCGGAGATTGCCGACGCGCGCTGCTTCTGCTGCTGAGGTCACCGGCTGTAT 7438
Qy 61 LeuAapAapAapProLeuValIysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
Db 7437 TTG-----CGCGTGTCTTCACTGCTGCTGAGGCGCGCGCTTGTCCGAGTTG 7384
Qy 81 IleAlaGlnValHis-----AenHisGlnAlaLysGlyGlyLeuIleLeuGln 96
Db 7383 AGGCGGAGCTGAGGCGCTGGCGCGCGTGAAGG-GCGCGAGCGCGTGCATCGAGGCT 7325
Qy 97 Gly-----GlySerIleSerLeuLeuArgCysMetAlaGlnSerArg 110
Db 7324 GCGGAGGTGACCGCGAGACGCGCGCA-AGCTTCTCTCCG-----AGG 7281
Qy 111 TyrTPAaAlaAapPhe---ArgTPHsiIleIleArgAsnGlnLeuAlaAapGlnGlu 129
Db 7280 ACCTGATCGCGCTCATCCGCGGCTGAGATTCAATCGGACAGGCG-GTGCCCGCTCG 7222
Qy 130 SerPheMetSerValAlaLysThrArgValIysGlnMetLeuArgProSerAlaGlyLeu 149
Db 7221 GCGTTC-----CGAAGGCCCATGCGCTTC 7198
Qy 150 SerIleIleGlnGlnLeuValGlnLeuTPArgGluProArgLeuArgProIleLeuGln 169
Db 7197 GCGCGGAGCGGTATCCCTTCACATGTAAGTTCGTGTGCCACCGCGGACGTCGTATC 7138
Qy 170 GlyIleAapGlyTyrArgTyrAlaLeuLeuPheAlaThr---GlnAsnGlnIleThrPro 188
Db 7137 GGGCTCATATCACACGCGACGCGGATGTTCTGAGCGTGGCTGTCAGAGAGACCCGC 7078
Qy 189 AapMetLeu-----LeuGln 193
Db 7077 GAGCTGCTGGCGCGCGGCGGATGCCCATTCGCGCCCATGCGAGCGTGGCTATGTCCAG 7018
Qy 194 LeuAapAlaAapMetGlnAanLysLeu-----IleHisGlyIleAlaGln 208
Db 7017 GCGCGCGCGCTGTTGAGGGGCGGATGACGCGGAAAGAGGCAATTCACGACCGCGCG 6958
Qy 209 GlnPheLeuIleHisAlaArgArgGln-----GlnGlnLysPheProLeuValGly 225
Db 6957 GAGACGCGCGCTAGCGCAAGCGGAGTTGACGTGTCTCCGGAAGAGAGCC-----GGG 6904
Qy 226 AlaThrAlaValGlnAlaPheGlnGlyProPhe 237
Db 6903 GCT-----GTTCTTCTGGCTCCCGGTCAC 6880

RESULT 15
US-09-602-787A-277
Sequence 277, Application US/09602787A
Patent No. 6696561
GENERAL INFORMATION:
APPLICANT: Pompeius, Mark
APPLICANT: Krüger, Burkhard
APPLICANT: Schöder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932182.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932190.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932191.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932229.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932927.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940766.5
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PRIOR FILING DATE: 1999-08-27
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PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940833.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941395.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942077.7
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942078.5
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942079.3
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 678
SEQ ID NO 277
LENGTH: 1026
TYPE: DNA
ORGANISM: Corynebacterium glutamicum

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FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1003)
; OTHER INFORMATION: RXS02228
US-09-602-787A-277
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Alignment Scores:
Pred. No.: 0.00173 Length: 1026
Score: 110.00 Matches: 43
Percent Similarity: 43.7% Conservative: 33
Best Local Similarity: 24.7% Mismatches: 72
Query Match: 8.9% Indels: 26
DB: 3 Gaps: 5
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US-10-817-483-2 (1-239) x US-09-602-787A-277 (1-1026)

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QY 6 ILePheGlyProThrCysThrGlySerThrAlaIleAlaLeuAlaGlnInthr 25
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 GTGTTGGACCCACCTGCATCTGGAAACACGCTTGGGAATTGCTAGCCACAGCCT 178
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 26 GlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrGlySer 45
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 GACGCTGAAGTACATGATGATGATTCATGACGCTGACAAAGGACATCGGCACG 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 46 GlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyrLeuAspArgPro 65
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 GCAAAAGCTGACTGTGAAAGACGCGAAGCATTCGGCATCATCAGCTGATGCTCGGAC 298
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 66 LeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeuIleAlaValHis 85
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 GTTACCGAACTGGCGTCAGTGGCGAGGTTTCATCCGAC--GCCGTTCCGATGTGAA 355
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 86 AsnHisGluAlaLysGlyGlyLeu--IleLeuGlnGlyGlySerIleSerLeuLeuArg 104
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 GATATTATGTCCTCGGCAAAACCCCATCTGTGGCGGCTCCATGTTGTACGTCCTCAA 415
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 105 CysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIleIleArgAsnGlu 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 416 -----TCT 418

QY 125 LeuAlaAspGlnGlnSerPheMet-----SerValAlaLysThrArgValLysGln 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 419 TTGTCGATGATGGCATTTCCACCTACCGACGAGCGCTGTTCCGCGACGCTTGAGGCC 478
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 142 MetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArgGlu 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 479 CGCTTGGCAGACATCGTGTGCAAGCACTACACGCTGAACCTTACTCAGCTT-----GAC 532
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 162 ProArgLeuArgProIleLeuGlnGlyLysAspGlyTyrArg 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 533 CCAAGAACGACGACCGCTCATCGAAAGCAATGATCCCGACGC 574
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: June 26, 2006, 21:05:16
Job time : 212 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 20:05:52 ; Search time 1277 Seconds
(without alignments)

3449.583 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
Sequence: 1 MDRLRIFGPTGTGKTSTAIA.....KPLVGAIVAEAFEGPPPM 239

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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-DB=Published_Applications_NA_Main -QFMT=fastap -SUPPLX=p2n.rnpbm
-MINMATCH=0.1 -LOOPEL=50 -LOOPEXT=0 -LIST=bits -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcio -NORM=ext
-HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abses05h
-USER=US10817483 @CGN 1.1 1675 @runat.26062006.142803.19017 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

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3: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Ceitera_SIDS3/prodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1230	100.0	717	7	US-10-369-493-38935

2	1230	100.0	723	7	US-10-409-701-2	Sequence 2, Appli
3	1230	100.0	1919	9	US-10-817-483-1	Sequence 1, Appli
4	1230	100.0	2722	13 <td>US-11-139-461-8</td> <td>Sequence 8, Appli</td>	US-11-139-461-8	Sequence 8, Appli
5	1230	100.0	2722	13 <td>US-11-139-461-9</td> <td>Sequence 9, Appli</td>	US-11-139-461-9	Sequence 9, Appli
6	1230	100.0	3017	13 <td>US-11-139-461-12</td> <td>Sequence 12, Appli</td>	US-11-139-461-12	Sequence 12, Appli
7	1230	100.0	5622	7 <td>US-11-139-461-7</td> <td>Sequence 7, Appli</td>	US-11-139-461-7	Sequence 7, Appli
8	1075	87.4	720	7 <td>US-10-369-493-35042</td> <td>Sequence 35042, A</td>	US-10-369-493-35042	Sequence 35042, A
9	1075	87.4	720	7 <td>US-10-369-493-38138</td> <td>Sequence 38138, A</td>	US-10-369-493-38138	Sequence 38138, A
10	1075	87.4	720	7 <td>US-10-369-493-38549</td> <td>Sequence 38549, A</td>	US-10-369-493-38549	Sequence 38549, A
11	1075	87.4	720	7 <td>US-10-369-493-38954</td> <td>Sequence 38954, A</td>	US-10-369-493-38954	Sequence 38954, A
12	1075	87.4	723	16 <td>US-10-821-711-2</td> <td>Sequence 2, Appli</td>	US-10-821-711-2	Sequence 2, Appli
13	1068	86.8	723	16 <td>US-11-156-084-1</td> <td>Sequence 1, Appli</td>	US-11-156-084-1	Sequence 1, Appli
14	1068	86.8	723	16 <td>US-11-156-084-20</td> <td>Sequence 20, Appli</td>	US-11-156-084-20	Sequence 20, Appli
15	1066	86.7	720	7 <td>US-10-369-493-38969</td> <td>Sequence 38969, A</td>	US-10-369-493-38969	Sequence 38969, A
16	1052	85.5	720	7 <td>US-10-369-493-38968</td> <td>Sequence 38968, A</td>	US-10-369-493-38968	Sequence 38968, A
17	1052	85.5	1997	8 <td>US-10-465-008-1</td> <td>Sequence 1, Appli</td>	US-10-465-008-1	Sequence 1, Appli
18	1050	85.4	720	7 <td>US-10-369-493-38949</td> <td>Sequence 38949, A</td>	US-10-369-493-38949	Sequence 38949, A
19	1050	85.4	720	7 <td>US-10-369-493-38953</td> <td>Sequence 38953, A</td>	US-10-369-493-38953	Sequence 38953, A
20	1050	85.4	723	16 <td>US-11-156-084-16</td> <td>Sequence 16, Appli</td>	US-11-156-084-16	Sequence 16, Appli
21	1050	85.4	723	16 <td>US-11-156-084-18</td> <td>Sequence 18, Appli</td>	US-11-156-084-18	Sequence 18, Appli
22	1035	84.1	777	7 <td>US-10-369-493-38971</td> <td>Sequence 38971, A</td>	US-10-369-493-38971	Sequence 38971, A
23	1005	81.7	720	7 <td>US-10-369-493-38936</td> <td>Sequence 38936, A</td>	US-10-369-493-38936	Sequence 38936, A
24	1005	81.7	720	7 <td>US-10-369-493-38940</td> <td>Sequence 38940, A</td>	US-10-369-493-38940	Sequence 38940, A
25	1005	81.7	720	7 <td>US-10-369-493-38964</td> <td>Sequence 38964, A</td>	US-10-369-493-38964	Sequence 38964, A
26	1005	81.7	720	7 <td>US-10-369-493-38966</td> <td>Sequence 38966, A</td>	US-10-369-493-38966	Sequence 38966, A
27	1005	81.7	723	6 <td>US-10-187-339-12</td> <td>Sequence 12, Appli</td>	US-10-187-339-12	Sequence 12, Appli
28	1005	81.7	1988	8 <td>US-10-363-723-2</td> <td>Sequence 2, Appli</td>	US-10-363-723-2	Sequence 2, Appli
29	1005	81.7	2595	7 <td>US-10-369-324-3</td> <td>Sequence 3, Appli</td>	US-10-369-324-3	Sequence 3, Appli
30	1005	81.7	2595	8 <td>US-10-392-301-3</td> <td>Sequence 3, Appli</td>	US-10-392-301-3	Sequence 3, Appli
31	1005	81.7	2595	9 <td>US-10-607-538-3</td> <td>Sequence 3, Appli</td>	US-10-607-538-3	Sequence 3, Appli
32	1005	81.7	2595	9 <td>US-10-667-145-3</td> <td>Sequence 3, Appli</td>	US-10-667-145-3	Sequence 3, Appli
33	1005	81.7	2595	10 <td>US-10-505-079-3</td> <td>Sequence 3, Appli</td>	US-10-505-079-3	Sequence 3, Appli
34	1005	81.7	9323	7 <td>US-10-369-324-4</td> <td>Sequence 4, Appli</td>	US-10-369-324-4	Sequence 4, Appli
35	1005	81.7	9323	10 <td>US-10-607-538-4</td> <td>Sequence 4, Appli</td>	US-10-607-538-4	Sequence 4, Appli
36	1005	81.7	9323	10 <td>US-10-505-079-4</td> <td>Sequence 4, Appli</td>	US-10-505-079-4	Sequence 4, Appli
37	994	80.8	747	6 <td>US-10-187-339-5</td> <td>Sequence 5, Appli</td>	US-10-187-339-5	Sequence 5, Appli
38	984	80.0	3183	7 <td>US-10-072-077A-1</td> <td>Sequence 1, Appli</td>	US-10-072-077A-1	Sequence 1, Appli
39	984	80.0	3183	15 <td>US-11-154-865-1</td> <td>Sequence 1, Appli</td>	US-11-154-865-1	Sequence 1, Appli
40	826	67.2	559	7 <td>US-10-369-493-37835</td> <td>Sequence 37835, A</td>	US-10-369-493-37835	Sequence 37835, A
41	686.5	55.8	2544	6 <td>US-10-187-339-9</td> <td>Sequence 9, Appli</td>	US-10-187-339-9	Sequence 9, Appli
42	605.5	49.2	729	7 <td>US-10-369-493-38941</td> <td>Sequence 38941, A</td>	US-10-369-493-38941	Sequence 38941, A
43	603.5	49.1	729	7 <td>US-10-369-493-38946</td> <td>Sequence 38946, A</td>	US-10-369-493-38946	Sequence 38946, A
44	603.5	49.1	729	7 <td>US-10-369-493-38270</td> <td>Sequence 38270, A</td>	US-10-369-493-38270	Sequence 38270, A
45	603.5	49.1	729	7 <td>US-10-369-493-38608</td> <td>Sequence 38608, A</td>	US-10-369-493-38608	Sequence 38608, A

ALIGNMENTS

RESULT 1
US-10-369-493-38935
; Sequence 38935, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38935
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; US-10-369-493-38935
Alignment Scores:

Pred. No.: 3.78e-149 Length: 717
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-817-483-2 (1-239) x US-10-369-493-38935 (1-717)

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OY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGATCTACGCTCTAATTTTCGGTCCACTTGACAGAGAAAGACATCGACTGCATAGCT 60
OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTTCGCCAGCAGACTGGCTCCCTCCAGTCTCTCGCTCGATCGCATGCTCAATGCTCTCAA 120
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThrArgLeuTyr 60
DB 121 CTATCAACCGAAGCGGGCGACCAACAGTGAAGAACTGAAAGAACAGACTCGTCTATC 180
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
DB 181 CTGATGATCCCTTTGGTAAAGGATCATTAACGCCCAAGCAAGCTCATGAACGGCTC 240
OY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyIleLeuGlnGlnGlySerIle 100
DB 241 ATTCGGAGGATGCAACATCAAGAGCGCAAGCGGGCTTATCTTGAAGGAGATCATTC 300
OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAGAGTGCATGCGCCCAAGTCTTATTTGGAACCGCGATTTTCGTTGGCATTT 360
OY 121 IleArgAsnGluLeuAlaAspGlnGlnSerPheMetSerValAlaLysThrArgValLys 140
DB 361 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCGGCCAAGCCAGAGTTAAG 420
OY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTCTGCAGGCTTCTTATTAACAAGATGGTTCACACTTGGAGG 480
OY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCTCGGCTGAGGCGCATCTGGAAGGATCGATGATTCATATGATGCGCTGCTATTT 540
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
DB 541 GCTACCCAGAACCGATCAAGATCAGCCCGATGTGCTATTGACAGCTCGACGAGATATGAGAA 600
OY 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
DB 601 AAATTGATTACCGGTATCGCTCAGAGTTTCTTAATTCATGCGCGTTCAGAGAACAGAA 660
OY 221 PheProLeuValGlyAlaThrAlaValAlaPheGlnGlyProProPheArgMet 239
DB 661 TTCCTTTGGTGGGCGGACAGCTGTGAAAGCGTTTGAAGCAACCATTTGCAATG 717
```

RESULT 2

US-10-409-701-2
; Sequence 2, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Helenjarris, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exscretion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

LENGTH: 723
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(720)
US-10-409-701-2

Alignment Scores:

Pred. No.: 3.82e-149 Length: 723
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-817-483-2 (1-239) x US-10-409-701-2 (1-723)

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OY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGATCTACGCTCTAATTTTCGGTCCACTTGACAGAGAAAGACATCGACTGCATAGCT 60
OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTTCGCCAGCAGACTGGCTCCCTCCAGTCTCTCGCTCGATCGCATGCTCTCAATGCTCTCAA 120
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThrArgLeuTyr 60
DB 121 CTATCAACCGAAGCGGGCGACCAACAGTGAAGAACTGAAAGAACAGACTCGTCTATC 180
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
DB 181 CTGATGATCCCTTTGGTAAAGGATCATTAACGCCCAAGCAAGCTCATGAACGGCTC 240
OY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyIleLeuGlnGlnGlySerIle 100
DB 241 ATTCGGAGGATGCAACATCAAGAGCGCAAGCGGGCTTATCTTGAAGGAGATCATTC 300
OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAGAGTGCATGCGCCCAAGTCTTATTTGGAACCGCGATTTTCGTTGGCATTT 360
OY 121 IleArgAsnGluLeuAlaAspGlnGlnSerPheMetSerValAlaLysThrArgValLys 140
DB 361 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCGGCCAAGCCAGAGTTAAG 420
OY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTCTGCAGGCTTCTTATTAACAAGATGGTTCACACTTGGAGG 480
OY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCTCGGCTGAGGCGCATCTGGAAGGATCGATGATTCATATGATGCGCTGCTATTT 540
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
DB 541 GCTACCCAGAACCGATCAAGATCAGCCCGATGTGCTATTGACAGCTCGACGAGATATGAGAA 600
OY 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
DB 601 AAATTGATTACCGGTATCGCTCAGAGTTTCTTAATTCATGCGCGTTCAGAGAACAGAA 660
OY 221 PheProLeuValGlyAlaThrAlaValAlaPheGlnGlyProProPheArgMet 239
DB 661 TTCCTTTGGTGGGCGGACAGCTGTGAAAGCGTTTGAAGCAACCATTTGCAATG 717
```

RESULT 3

US-10-817-483-1
; Sequence 1, Application US/10817483
; Publication No. US20040237147A1
; GENERAL INFORMATION:
; APPLICANT: Haben, Jeffrey E.
; APPLICANT: Zinselmeier, Christopher

```

; APPLICANT: Tomes, Dwight
; APPLICANT: Abbitc, Shane
; APPLICANT: Helentjaris, Timothy G.
; APPLICANT: Niu, Xiaomu
; TITLE OF INVENTION: Modulation of cytokinin Activity in
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 0803R
; CURRENT APPLICATION NUMBER: US/10/817,483
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/460,718
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 09/545,334
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1919
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (690)..(1411)
; OTHER INFORMATION: Ipc
; US-10-817-483-1

```

Alignment Scores:

```

Pred. No.: 1,57e-148 Length: 1919
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

```

US-10-817-483-2 (1-239) x US-10-817-483-1 (1-1919)

```

QY 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleala 20
DB 690 ATGATCTACGCTCTAATTTTCGGTCCAACTTCACAGAAAGACATCGACTCGATAGCT 749
QY 21 LeuIaGInGInThGlyLeuProValLeuSerLeuAapArgValGInCysCysProGIn 40
DB 750 CTGGCCAGACAGACTGGCTCCACAGTCTCTGCTGATCGGCTCAATGCTGCTCA 809
QY 41 LeuSerThrGlySerGlyArgProThrValGInGInLeuLysGlyThrThraArgLeuTy 60
DB 810 CTATCAACCGGAAGCGGGGAGCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 869
QY 61 LeuAapAapArgProLeuValLysGlyIleIleThraIalysGInAlaHisGInuArgLeu 80
DB 870 CTGTATGATCGCCCTTTGGTAAAGGTATCATTAACAGCCAAAGCTCATGAAAGCGCTC 929
QY 81 IleIaGInValHisAsnHisGInuAlaLysGlyLysLeuIleLeuGInGlyLysSerIle 100
DB 930 ATTGGAGAGGTGCAAAATCAAGAGCCAAAGCGGCTTATCTTGAAGGAGATCTATC 989
QY 101 SerLeuLeuArgCysMetAlaGInSerArgTyrrTPAsnAlaAapPheArgTrpHisIle 120
DB 990 TCGTTGCTCAGGTGCATGGCGCAAGTCTTATTTGGAAGCGCGATTTTCTTGGCATATT 1049
QY 121 IleArgAaGInLeuAlaAapGInGInLeuSerPheMetSerValAlaLysThrArgValLys 140
DB 1050 ATTCACAAGAGTGTACAGACAGAGAGCTTCATGAGCGGTGGCCAAAGCCAGAGTTAAG 1109
QY 141 GInMetLeuArgProSerAlaGlyLeuSerIleIleGInGInLeuValGInLeuTrpArg 160
DB 1110 CAGATGTTACGCCCTCTGCAAGTCTTCTATTAATCAAGAGTTGTTCAACTTTGGAGG 1169
QY 161 GInProAlaArgLeuArgProIleLeuGInGlyIleAapGlyTyrrArgTyrrAlaLeuLeuPhe 180
DB 1170 GAGCTCGGCTGAGGCGCCATCTGGAAGGATCGATGATATCGATATGCCCTGCTATT 1229

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```

QY 161 AlaThrGInaGInIleIleThrProAspMetLeuLeuGInLeuAapAlaAapMetGInuAsn 200
DB 1230 GCTACCCGGAACCAATACACGCCCTCATATGCTATTGACGCTCGACGAGATATGGAAT 1289
QY 201 LysLeuIleHisGlyTleAlaGInGInLeuPheLeuIleHisAlaArgArgGInGInLys 220
DB 1290 AAATTGATTCACGAGTATGCTCTCAGAGATTTCTAATCCATTCGCCGCTCGACAGAACAGAA 1349
QY 221 PheProLeuValGlyAlaIleThraIalValaPheGInGlyProProPheArgMet 239
DB 1350 TTCCCTTGTGGGGCGACAGCTGTGAAAGCGTTTGAAGACCAATTTGGAATG 1406

```

RESULT 4

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US-11-139-461-8
; Sequence 8, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; TITLE OF INVENTION: Seeds
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Hordeum vulgare, Plant Journal 6:849-860
; OTHER INFORMATION: (1994); gene from Agrobacterium tumefaciens, Molecular
; OTHER INFORMATION: and General Genetics 216:388-394 (1989); terminator
; OTHER INFORMATION: from Zea mays, Genbank Accession #S78780.
; US-11-139-461-8

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Alignment Scores:

```

Pred. No.: 2.6e-148 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

```

US-10-817-483-2 (1-239) x US-11-139-461-8 (1-2722)

```

QY 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleala 20
DB 1525 ATGATCTACGCTCTAATTTTCGGTCCAACTTCACAGAAAGACATCGACTCGATAGCT 1584
QY 21 LeuIaGInGInThGlyLeuProValLeuSerLeuAapArgValGInCysCysProGIn 40
DB 1585 CTGGCCAGACAGACTGGCTCCACAGTCTCTGCTGATCGGCTCAATGCTGCTCA 1644
QY 41 LeuSerThrGlySerGlyArgProThrValGInGInLeuLysGlyThrThraArgLeuTy 60
DB 1645 CTATCAACCGGAAGCGGGGAGCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 1704
QY 61 LeuAapAapArgProLeuValLysGlyIleIleThraIalysGInAlaHisGInuArgLeu 80
DB 1705 CTGTATGATCGCCCTTTGGTAAAGGTATCATTAACAGCCAAAGCTCATGAAAGCGCTC 1764
QY 81 IleIaGInValHisAsnHisGInuAlaLysGlyLysLeuIleLeuGInGlyLysSerIle 100
DB 1765 ATTGGAGAGGTGCAAAATCAAGAGCCAAAGCGGCTTATCTTGAAGGAGATCTATC 1824
QY 101 SerLeuLeuArgCysMetAlaGInSerArgTyrrTPAsnAlaAapPheArgTrpHisIle 120
DB 1825 TCGTTGCTCAGGTGCATGGCGCAAGTCTTATTTGGAAGCGCGATTTTCTTGGCATATT 1884

```

QY 121 lIeaRgaNglUleuAlaSPglUSeRPhemeSeRValAlaYsThrArYVallys 140
|||
Db 1885 ATTGCACAGAGTTAGAGAGAGAGAGGCTTCAAGCGCGGACAGACCAAGGTTAAAG 1944
QY 141 GlmUetleuArPProSeRAlaGlyLeuSeRlleIlegInglUleuValGlnLeuTrpArg 160
|||
Db 1945 CAGATGTTACGCCCCCTCTGACAGGTCCTTCTATTATCCAGAGTTGGTTCACTTTGGAGG 2004
QY 161 GluProArGleuArPProIleleuGlnGlylleaSPgLyTyRArgTyRAlaLeuLeuPhe 180
2005 GAGCCTGGGCTGAGGCCCATCTGAGAGGATCGATGATATCGATATGCCCTCTATT 2064
QY 181 AlAthrgInaNgInlleThrProaSPMeCleuLeuGlnLeuAspAlaSPMeCleuGln 200
2065 GCTACCCAGAACAGATCACGCCCGCATATGCTATTGCGCTCGACGCGAGATATGAGAA 2124
QY 201 lYsleuIleHISgLyIleAlaGlnGluPheleuIleHISAlaArGArGInglUlns 220
2125 AAATTGATTACGGTATCGCTCAGAGATTCTTAATTCATGCGCGCTCGACAGAAACAGAA 2184
QY 221 PheProleuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArGMe 239
2185 TTCCTTTGGTGGGCGGACAGCTGTGGAAGCGTTTGAAGACCACTTCGATG 2241
Db

RESULT 5

US-11-139-461-9
; Sequence 9, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinsmeister, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648;
; OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989); terminator from Solanum
; OTHER INFORMATION: tuberosum, Plant Cell 1(1):115-122 (1989).
US-11-139-461-9

Alignment Scores:

Pred. No.: 2,66-148 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) x US-11-139-461-9 (1-2722)

QY 1 MetAsePleuArGleuIlePheGlyProThrCySthrgLyIysThrSerThAlaIleAla 20
Db 1525 ATGATCTACGCTTAATTTTCGATCCACACTGCACAGAAAGACATGACATGAGTACT 1584
QY 21 leuAlaGInglInThrgLyLeuProValleuSeRleuAspArGValGlnCyCySPProGln 40
Db 1585 CTTCCCAAGACAGACTGGCTCCCGATCTCTGCTCGATCGCGTCGAATGCTGCTCTCAA 1644
QY 41 leuSerThrgLySerGlyArGProThrValGlnGluLeuLySgLyThrThArGleuTyR 60
|||

Db 1645 CTATCACCGGAAGCGGGGACCAACAGTGGAGAAGACTGAAGAGACGACTGCTGTAC 1704
QY 61 leuAspArGProleuValLySgLyIlelleThrAlaLySgInAlaHISgLyArGleu 80
|||
Db 1705 CTTGATATGCGCCCTTTGGTAAAGGTTATCATTAACCAAGCAAGCTCATGAGCGCTC 1764
QY 81 lIeAlaGlnAlaHISaNHISgLyAlaLySgLyIleuIleuGlnGlyIleuSerlle 100
1765 ATTGCGGAGGTGACCAATCACAGAGCCAAAGGCGGCTTATCTTGAGAGAGATCTATC 1824
QY 101 SerleuLeuArGcYsMeAlaGlnSerArGTyrTrpAsnAlaSPPheArGTyrPheAla 120
1825 TCGTTGCTCAGGTCATGCGGCAAAAGCTTATTTGAACCGGATTTTCGTTGCAATATT 1884
QY 121 lIeaRgaNglUleuAlaSPglUSeRPhemeSeRValAlaYsThrArYVallys 140
1885 ATTGCACAGAGTTAGAGAGAGAGAGGCTTCAAGCGCGGACAGACCAAGGTTAAAG 1944
QY 141 GlmUetleuArPProSeRAlaGlyLeuSeRlleIlegInglUleuValGlnLeuTrpArg 160
1945 CAGATGTTACGCCCCCTCTGACAGGTCCTTCTATTATCCAGAGTTGGTTCACTTTGGAGG 2004
QY 161 GluProArGleuArPProIleleuGlnGlylleaSPgLyTyRArgTyRAlaLeuLeuPhe 180
2005 GAGCCTGGGCTGAGGCCCATCTGAGAGGATCGATGATATCGATATGCCCTCTATT 2064
QY 181 AlAthrgInaNgInlleThrProaSPMeCleuLeuGlnLeuAspAlaSPMeCleuGln 200
2065 GCTACCCAGAACAGATCACGCCCGCATATGCTATTGCGCTCGACGCGAGATATGAGAA 2124
QY 201 lYsleuIleHISgLyIleAlaGlnGluPheleuIleHISAlaArGArGInglUlns 220
2125 AAATTGATTACGGTATCGCTCAGAGATTCTTAATTCATGCGCGCTCGACAGAAACAGAA 2184
QY 221 PheProleuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArGMe 239
2185 TTCCTTTGGTGGGCGGACAGCTGTGGAAGCGTTTGAAGACCACTTCGATG 2241
Db

RESULT 6

US-11-139-461-12
; Sequence 12, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinsmeister, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 3017
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, Genbank Accession #L22344;
; OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and
; OTHER INFORMATION: General Genetics 216:388-394 (1989); terminator from
; OTHER INFORMATION: Zea mays, Genbank Accession #L22345.
US-11-139-461-12

Alignment Scores:

Pred. No.: 3,07e-148 Length: 3017
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) X US-11-139-461-12 (1-3017)

OY	1	MetAspLeuArgLeuIleIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleIle	20
Db	1408	ATGGATCTACGTCCTAATTTTCGGTTCACCTTGACAGGAAAGACATCGACCTGATCT	146
OY	21	LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysAspProGln	40
Db	1468	CTTGCCACGACGACTGGCTCCAGTCCCTCGCTCGATCGGTCATATGGCTGCTCA	1527
OY	41	LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuThr	60
Db	1528	CTATCAACCCGGAAGCGGGCGACCAACAGTGGAAACATCGAAAGAACACTGCTGTAC	1587
OY	61	LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnAspArg	80
Db	1588	CTTGATGATCCGCTTGTGTAAAGGGATTCATTACAGCCAAAGCAAGCTCATAGAACGGCTC	1647
OY	81	IleAlaGluValHisAsnHisGlnValaLysGlyGlyLeuIleLeuGlnGlyGlySerIle	100
Db	1648	ATTGGGAGGTCGACAAATCAGAGGCGCAAAGCGGGCTTATCTTGAAGAGAGATCTATC	1707
OY	101	SerLeuLeuAspArgCysMetAlaGlnSerArgIleTyrTrpAsnAlaAspPheArgTrpHisIle	120
Db	1708	TCGTTGTCACAGGTGATGAGCGCAAGTGCATTATGGAAACGGGATTTTCGTTGGCATATT	1767
OY	121	IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaLysThrArgValLys	140
Db	1768	ATTGGCAACGAGTTAGACAGACGAGGAGCTTCATCAGACCGTGGCCCAACACGAGTTAAG	1827
OY	141	GlnMetLeuAspProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg	160
Db	1828	CAGATGTTACGCCCTCTGCAGAGTCTTTCTATTATCCAAAGTTGCTTCAACTTTGGAGG	1887
OY	161	GluProArgLeuAspArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe	180
Db	1888	GAGCTCGCGCTGAGGCGCATATCGAAGAGATCGATGATATCGATATGCGCTCGTATTT	1947
OY	181	AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn	200
Db	1948	GCTACCCCGAAGACAGATACAGCCCGCATATGCTATTGCAGCTCGAAGCAGATATGGAGAT	2007
OY	201	LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys	220
Db	2008	AAATTGATTCCACGGTATGCTCAGGAGTTTCTTAACTCATGGCGCTCGACAGAAACAGAA	2067
OY	221	PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet	239
Db	2068	TTCCCTTTGGTGGCGCGACACTGTCTCAAGCGTTTGAAGACACCACTTCGATG	2124

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; OTHER INFORMATION: Promoter and terminator from Zea mays as found in
; OTHER INFORMATION: Genbank Accession #S78780; gene from Agrobacterium
; OTHER INFORMATION: tumefaciens as found in Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989) .
US-11-139-461-7

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Alignment Scores:

Pred. No.:	7,42e-148	Length:	5622
Score:	1230.00	Matches:	239
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	13	Gaps:	0

US-10-817-483-2 (1-239) X US-11-139-461-7 (1-5622

Qy	1	Metaspneuargleu1lephg1yProThrCysThrGlyLysThrSerThrAla1lela	20
Db	1525	ATGGATCTACGCTCTAAATTTTCGGTCCAACTTGCAACAGGAAGAACATCGACTGCGATTACT	158
Qy	21	LeuAlaIngInthrGlyLeuProValLeuSerLeuAspArgValGlnCysAspProGln	40
Db	1585	CTTGCCCGACGAGCATGGCGTCTCCAGTCCCTCGCTCGATCGCGTCCAAATGCTGTCCTCAA	164
Qy	41	LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThrArgLeuTyr	60
Db	1645	CTATCAACCCGAAACGGGGCGACCAACGTGGAACACTGAAGAAACACATCTGCTGTAC	170
Qy	61	LeuAspAspArgProLeuValLysGlyVileIleThrAlaLysGlnAlaHisGlnArgLeu	80
Db	1705	CTTATGATATGCCCTTTTGCTTAAGGATATCTATTACGCCAAGCAAGCTCATGAACGGCTC	176
Qy	81	IlleAlaGlnValHisAsnHisGlnAlaLysGlyGlyLeuIleLeuGlnGlyGlySerIle	100
Db	1765	ATTCCGAGAGGTGCACAATTCACGAGGCCAAAGCGCGCTTATCTTGAGGGAGATCTATTC	182
Qy	101	SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle	120
Db	1825	TGCTTGCTCAGGTGCATAGCGCCAAAGTCGTTATTGGAACCGCGGATTTTCGTTGGCATATT	188
Qy	121	IleArgAsnGlnLeuAlaAspGlnGlnLysSerPheMetSerValAlaLysThrArgValLys	140
Db	1885	ATTGCGAACAGGATTAGCAGACGAGAGAGGCTTCATGAGCGTGCGCAAGACCAGATTAAAG	194
Qy	141	GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg	160
Db	1945	CAGATGTTAGCGCCCTCTGCAGGCTCTTCAATTATCCAAAGATGGTTCAACTTGGAGGG	200
Qy	161	GlnProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe	180
Db	2005	GAGCTTCGGCTGAGGCCCATCTCTGGAAGGATGATGATATCATATGCTCTCTATTT	206
Qy	181	AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn	200
Db	2065	GCTACCCAGAACCGATGATCAGCGCCGATATGCTATTGACGCTCGACGACGATATGAGCAAT	212
Qy	201	LysLeuLeuIleHisGlyIleAlaGlnGlnPheLeuLeuHisAlaAspArgGlnGlnGlnLys	220
Db	2125	AAATTTGATTCACGGATATCGCTCAGGAGCTTCTAATTCATGGCGCTTCACAGGAACAGAA	218
Qy	221	PheProLeuValGlyAlaTrnAlaValaGlnAlaPheGlnGlyProProPheArgMet	239
Db	2185	TTCCCTTTTGGTGGGCGGACAGCGTGTGGAAGCGTTTGAAGGACCACTTTCGATG	224
RESULT 8			
US-10-369-493-35042			
; Sequence 35042, Application US/10369493			
; Publication No., US20030233675A1			
; GENERAL INFORMATION:			
; APPLICANT: Cao, Yongwei			
; APPLICANT: Hinkle, Gregory J.			
; APPLICANT: Slater, Steven C.			
; APPLICANT: Goldman, Barry S.			

```
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35042
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-35042

Alignment Scores:
Pred. No.: 5,47e-129 Length: 720
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: Gaps: 7

US-10-817-483-2 (1-239) x US-10-369-493-35042 (1-720)

QY 1 MetaspleuAArgLeuIlePheGlyProThrCysThrGlyYstThrSerThrAlaIleAla 20
DB 1 ATGATCTGGCGTCAATTTCGGTCCAACTTGCAACAGAAAGACGTCAACCGCGTAGCT 60
QY 21 LeuAAGInGInThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTGCCCAGCAGACTGGGCTTCCAGTCTTCCGCTCGATCGGGTCCAAATGTTGCTCAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnLeuLeuYsglyYstThrArgLeuYr 60
DB 121 CTGTCACCGGAGAGCGAGCAGCAACAGTGGAAAGATGAAAGAGACGACCGCTATAC 180
QY 61 LeuAspAspArgProLeuValIlyGlyIleIleThrAlaIlyGlnAlaIleGluArgLeu 80
DB 181 CTTATGATCGGCTCTGGTGAAGGATATCGACGCAAGCAAGCTCATGAAAGGCTG 240
QY 81 IleAlaGluValHisAsnHisGluAlaIlyGlyLeuIleGluGlySerIle 100
DB 241 ATGGGGAGGTGTATATATATAGAGCCCAACGGCGGCTTATTTGAGGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAAGTGCATGCGCAAAAGCAGTTATGAGATGCGGATTTTCGTTGGCATATT 360
QY 121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaIleThrArgValIly 140
DB 361 ATGGCCAGAGGTATAGACAGAGAGAGCTTCATGAACGTGGCCAAAGCCAGATTAAAG 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACCCCTCGCTGCAAGGCTTTCTATTAACAAGATTGATCTTTGGAAA 480
QY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyYrArgYrAlaLeuLeuPhe 180
DB 481 GAGCTCGGCTGAGGCGCATACCTGAAGAAGATCGATGATATCGATATGCAATGTGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTAGCCAGAACCAAGATCAATCCGATATGCTATGAGCTTGAGAGCATATGAGAGAT 600
QY 201 LysLeuIleHisGlyIleAlaGlnIlePheLeuIleHisAlaArgArgGlnGlnIly 220
DB 601 AAGTTGATTCATGGATCGCTCAGAGATATCTCATCCATGCAAGCCGCAAGAACAGAAA 660
QY 221 PheProLeuValGlyAlaThrAlaValAlaPheGlnGlyIleProProPheArgMet 239
DB 661 TTCCTCGAGTTAACGACGCGCTTACGACGAGATTGAAAGGTATCATCTTCGGAATG 717
```

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RESULT 9
US-10-369-493-38138
; Sequence 38138, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38138
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38138

Alignment Scores:
Pred. No.: 5,47e-129 Length: 720
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: Gaps: 7

US-10-817-483-2 (1-239) x US-10-369-493-38138 (1-720)

QY 1 MetaspleuAArgLeuIlePheGlyProThrCysThrGlyYstThrSerThrAlaIleAla 20
DB 1 ATGATCTGGCGTCAATTTCGGTCCAACTTGCAACAGAAAGACGTCAACCGCGTAGCT 60
QY 21 LeuAAGInGInThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTGCCCAGCAGACTGGGCTTCCAGTCTTCCGCTCGATCGGGTCCAAATGTTGCTCAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnLeuLeuYsglyYstThrArgLeuYr 60
DB 121 CTGTCACCGGAGAGCGAGCAGCAACAGTGGAAAGATGAAAGAGACGACCGCTATAC 180
QY 61 LeuAspAspArgProLeuValIlyGlyIleIleThrAlaIlyGlnAlaIleGluArgLeu 80
DB 181 CTTATGATCGGCTCTGGTGAAGGATATCGACGCAAGCAAGCTCATGAAAGGCTG 240
QY 81 IleAlaGluValHisAsnHisGluAlaIlyGlyLeuIleGluGlySerIle 100
DB 241 ATGGGGAGGTGTATATATATAGAGCCCAACGGCGGCTTATTTGAGGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAAGTGCATGCGCAAAAGCAGTTATGAGATGCGGATTTTCGTTGGCATATT 360
QY 121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaIleThrArgValIly 140
DB 361 ATGGCCAGAGGTATAGACAGAGAGAGCTTCATGAACGTGGCCAAAGCCAGATTAAAG 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACCCCTCGCTGCAAGGCTTTCTATTAACAAGATTGATCTTTGGAAA 480
QY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyYrArgYrAlaLeuLeuPhe 180
DB 481 GAGCTCGGCTGAGGCGCATACCTGAAGAAGATCGATGATATCGATATGCAATGTGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTAGCCAGAACCAAGATCAATCCGATATGCTATGAGCTTGAGAGCATATGAGAGAT 600
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Oy      201  |ysleuileh|e|g|y|le|a|g|n|g|u|p|he|leu|l|e|h|s|l|a|a|a|g|g|n|g|u|l|n|y|s      220
Db      601  |AA|G|T|G|A|T|C|A|T|G|G|A|T|C|G|C|T|C|A|G|A|G|A|T|C|A|T|C|A|T|C|A|C|C|C|A|C|A|A|C|A|G|A|A      660
Oy      221  |phe|Pro|Leu|val|G|y|al|a|Thr|al|a|val|G|u|al|a|phe|G|n|g|u|l|Pro|Pro|P|he|a|r|Met      239
Db      661  |T|T|C|C|C|T|C|G|A|T|T|A|A|C|G|C|A|C|C|G|C|T|T|A|C|A|G|C|G|A|T|T|C|G|A|A|G|T|C|A|T|C|G|A|A|T|G      717

RESULT 10
US-10-369-493-38549
Sequence 38549, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 38549
LENGTH: 720
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38549

Alignment Scores:
Pred. No.:      5,47e-129      Length:      720
Score:          1075.00      Matches:      206
Percent Similarity: 93.7%      Conservative: 18
Best Local Similarity: 86.2%      Mismatches:  15
Query Match:    87.4%      Indels:      0
DB:              7      Gaps:         0

US-10-817-483-2 (1-239) x US-10-369-493-38549 (1-720)

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QY 1 MetAPLeuArgLeuIleIlePheGlyProThrCysThrGlyPheThrSerThrAlaIleA 20
Db 1 ATGATCTCGCGCTTAATTTTCCGATCCACTTGACAGAAAGACGTCGACCGCGTAGCT 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 61 CTGCGCCAGCAGACTCGGCGTTCCAGTCCTTTGGCTCGATCGGGTCCAAATGTTCTCTCAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuPheGlyThrThrArgLeuTyr 60
Db 121 CTGTCAACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGGAACGAGCGCTATAC 180
QY 61 LeuAspAspArgProLeuValIleGlyIleIleThrAlaIleGlnAlaIleGlnValGlu 80
Db 181 CTGTATGATCGGCTCTGTGTGAAGGTATCATCTGCAGCCAAAGCAAGCTCATGAAGGCTG 240
QY 81 IleAlaGlnValHisAsnHisGlnIleAlaIleGlyIleIleGlnGlnGlyGlySerIle 100
Db 241 ATGGGGGAGGCTATAATATATATAGAGCCACGGCGGGCTTAATCTTGAAGGAGGATTTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAACTGCATGCGCCGAAGCACTATATGAGAGTCGGATTTTCTTGCGCATATT 360
QY 121 IleArgGlnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaIleThrArgValIys 140
Db 361 ATTCGCCACGAGTTAGCAGACGAGGAGACCTTCATGAAGTGCGCCAAGCCAGAGTTAAG 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTyrArg 160

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Db      421  CAGAGTGTACGCCCTGCTGCAGAGCCCTTCTATATATCAAGAGTTGGTGTACTTTGGAAA 480
QY      161  GIuP-rOa-gLeuAtrProIleuGluGlyIleAsrGlyTYrArGTYrAlaLeuPhe 180
Db      481  GAGCCTCGCGCTGAGGCCCTCACTACTGAAAGAGTCGATGGAATATGCGATGTGTGTT 540
QY      181  AlArTrGInAsrGInIleThrProAspMetLeuLeuGInLeuAspAlaAspMetGluAsn 200
Db      541  GCTACCCAGAACCAATCATCATCCGATATGCTTATTCGAGCTTGACGAGATATGAGAGAT 600
QY      201  LysLeuIleHisGlyIleAlaGInGInPheLeuIleHisAlaArgArgInGInLys 220
Db      601  AAGTTGATTCAATGAGGATCGCTCAGAGGATCTCATTCATCCATCAGCCGACGAACAGAAA 660
QY      221  PheProLeuValGlyAlaThrAlaValAlaGluAlaPheGluGlyProProPheArgMet 239
Db      661  TTCCCTCGAGTTAACGCAAGCCGCTTACGACGAGATTGGAAGTCAATTCATTCGGAATG 717

RESULT 11
US-10-369-493-38954
; Sequence 38954, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38954
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38954

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Alignment Scores:		5.47e-129	Length:	720
Pred. No.:	Score:	1075.00	Matches:	206
	Percent Similarity:	93.7%	Conservative:	18
	Best Local Similarity:	86.2%	Mismatches:	15
	Query Match:	87.4%	Indels:	0
DB:		7	Gaps:	0

US-10-817-483-2 (1-239)	x	US-10-369-493-38954 (1-720)
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QY	1	MetAspLeuAArgLeuIlePheGlyProThrCysThrGlyLyThrSerThrAlaIleAla	20
Dp	1	ATGAACTCGCTAATTTTCGCTCAACTTGCAACAGGAAGAGCTGACCGCGTAGCT	60
QY	21	LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln	40
Dp	61	CTTGCCACGACAGCTGGGCTTCGACTCTTCGCTCGATCGGGTCCAAATTGTTCTTCAG	120
QY	41	LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr	60
Dp	121	CTGTCAACCGGAAGCGGACGACCAACGTGGAGAACTGAAGAAGAACGAGCGCTATAC	180
QY	61	LeuAspAspArgProLeuValLysGlyIleIleIleThrAlaLysGlnAlaHisGlnArgLeu	80
Dp	181	CTTGAAAGATCGGCTCTGTGGTGAAGGGTATCAATCCGACCAAGCAAGCTCATGAAGGCTG	240
QY	81	IleAlaGlnValHisAsnHisGlnAlaLysGlyLysLeuIleLeuGlnGlnGlySerIle	100
Dp	241	ATGGGGAGAGTGTATATATTAATTAAGAGCCACGCGCGGCTTATTTCTTAGAGGAGATCATC	300
QY	101	SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTyrPheHisIle	120

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Db 301 TCGTTGCTCAAGTGCATGCGCCAAAGCAAGTATTGGAGTGGCGATTTTCGTTGGCATATT 360
Qy 121 IleaarganglualeuAaSPgluGluSerPheMetSerValAlaIySerThArxValIys 140
Db 361 ATTGGCCAGAGTATGACAGACGAAAGACCTTCATGAACTGGCCAAAGCCAGAGTTAAG 420
Qy 141 GlnMetLeuAaSProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCCCTGCTGAGCGGCTTTCATATTCCAAAGAGTGGTTGATCTTTGGAAA 480
Qy 161 GluProArgLeuAaSProIleLeuGlnGlyIleAspGlyTrpArgTrpAlaLeuPhe 180
Db 481 GAGCTCGGCTGAGAGCCCATCTGAAAGACATCCATGATATCCATATGCCATGTGTT 540
Qy 181 AlaThrgInaengInIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTAGCCAGAACCAAGATCACAATCCGATATGCTATGACGCTTGACGAGATATGAGAGAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaIyArgGlnGlnIlys 220
Db 601 AAGTTGATTCATGGAGATCGCTCAGAGATATCTCATTCATGACGCGCAAGAAACAGAAA 660
Qy 221 PheProLeuValGlyAlaThraAlaValGluAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAACGACGCCGCTTACGACGATTCGAAGTTCATCCATTGCGAATG 717
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RESULT 12
US-10-821-711-2
; Sequence 2, Application US/10821711
; Publication No. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Elisia K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Mangsen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; TITLE OF INVENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 2
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-821-711-2
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Alignment Scores:
Pred. No.: 5,51e-129 Length: 723
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 9 Gaps: 0
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US-10-817-483-2 (1-239) x US-10-821-711-2 (1-723)

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Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrgIyLysTrSerThrAlaIleAla 20
Db 1 ATGATCTCGCGTCTAATTTTGGGTCCAACTTGCACAGAAAGACGTCAACCCGCGTACT 60
Qy 21 LeuAlaGlnGlnThrgIyLeuProValIleuSerLeuAspArgValGlnCysCyseProGln 40
Db 61 CTTGCCCGCAGACAGCTGGCTTCCAGTCTTCGCTCGATCGGTCGCAATGTTGGCTCAG 120
Qy 41 LeuSerThrgIySeGlyArgProThrValGlnGluLeuIyGlyThThArgLeuIyTr 60
Db 121 CTGTCAACCGGAGAGCGACCAACAGTTGAAAGAAAGCAAGCCGCTTATAC 180
Qy 61 LeuAspAspArgProLeuValIyGlyIleIleThraIyGlnIleHisGlyIyArgLeu 80
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Db 181 CTTATGATCGGCTCTGCTGTAAGAGTATCATGCCACCAAGCAAGCTCATGAAGAGCTG 240
Qy 81 IleaagluValHisasnhIsglyAlaIyGlyIleuGlnGlyIySerIle 100
Db 241 ATGGGAGAGGCTATTAATTTATGAGCCACGCGCGCTTATCTTGGAGGAGATCTATTC 300
Qy 101 SerLeuAspArgCysMetAlaGlnSerArgTrpTrpAspAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAAGTGCATGCGCCAAAGCAAGTATTGGAGTGGCGATTTTCGTTGGCATATT 360
Qy 121 IleaarganglualeuAaSPgluGluSerPheMetSerValAlaIySerThArxValIys 140
Db 361 ATTGGCCAGAGTATGACAGACGAAAGACCTTCATGAACTGGCCAAAGCCAGAGTTAAG 420
Qy 141 GlnMetLeuAaSProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCCCTGCTGAGCGGCTTTCATATTCCAAAGAGTGGTTGATCTTTGGAAA 480
Qy 161 GluProArgLeuAaSProIleLeuGlnGlyIleAspGlyTrpArgTrpAlaLeuPhe 180
Db 481 GAGCTCGGCTGAGAGCCCATCTGAAAGACATCCATGATATCCATATGCCATGTGTT 540
Qy 181 AlaThrgInaengInIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTAGCCAGAACCAAGATCACAATCCGATATGCTATGACGCTTGACGAGATATGAGAGAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaIyArgGlnGlnIlys 220
Db 601 AAGTTGATTCATGGAGATCGCTCAGAGATATCTCATTCATGACGCGCAAGAAACAGAAA 660
Qy 221 PheProLeuValGlyAlaThraAlaValGluAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAACGACGCCGCTTACGACGATTCGAAGTTCATCCATTGCGAATG 717
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RESULT 13
US-11-156-084-1
; Sequence 1, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; TITLE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; PRIOR FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
US-11-156-084-1
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Alignment Scores:
Pred. No.: 4,48e-128 Length: 723
Score: 1068.00 Matches: 205
Percent Similarity: 93.3% Conservative: 18
Best Local Similarity: 86.8% Mismatches: 16
Query Match: 86.8% Indels: 0
DB: 16 Gaps: 0
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US-10-817-483-2 (1-239) x US-11-156-084-1 (1-723)

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Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrgIyLysTrSerThrAlaIleAla 20
Db 1 ATGATCTCGCGTCTAATTTTGGGTCCAACTTGCACAGAAAGACGTCAACCCGCGTACT 60
Qy 21 LeuAlaGlnGlnThrgIyLeuProValIleuSerLeuAspArgValGlnCysCyseProGln 40
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Db 61 CTTGCCACAGACACTGGGCTTCACAGCTTCCTGCTGCATCGGAGTCCAAATTTCTCTCAG 120
Qy 41 LeuSerThnGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db 121 CTGTCAACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGGAACGAGCGGTATATC 180
Qy 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 181 CTTGATGATCGGCTCTGTGTGAAGGGTATCATCGACGCCAACAGCTCATGAAGGCTG 240
Qy 81 IleAlaGluValHisAsnHisGlnAlaLysGlyLysGlyLeuIleLeuGluGlySerIle 100
Db 241 ATGGGGGGGGGTATATATATATATAGAGCCGACGCGGCTTATTTCTGAGGAGAGATCTATC 300
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTPaAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAAGTGCATGCGCCGCAAGCAGTATTTGGAGTGGCGATTTTCTTGCGCATATT 360
Qy 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db 361 ATTCGCCACAGATTTAGCAGACGAAAGACCTTCATGAACTGGCCCAAGGCCAGAGTTAAG 420
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCTGCTGCTCAGAGCTTTCTATTTATTCAGAGTTGGTATCTTTGGAAA 480
Qy 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 481 GAGCTCGGCTGAGGCGCCACTACTGAAAGAGATCGATGATCGATATGCTCATGCTGTTGTT 540
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCAGAAACAGATCATCATCGATATGCTATGACCTTGACGCAATATGAGAGAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
Db 601 AAGTTGATTCATGGATGCTCAGAGATATCTCATTCATCATGACGCCGACAAAGACGAAA 660
Qy 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAAGCGAGCGGCTTACGACGAGATTCGAAGTTCATTCATTCGGAATG 717

RESULT 14

US-11-156-084-20
; Sequence 20, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (723)
US-11-156-084-20

Alignment Scores:

Pred. No.: 4 48e-128 Length: 723
Score: 1068.00 Matches: 205
Percent Similarity: 93.3% Conservative: 18
Best Local Similarity: 85.8% Mismatches: 16
Query Match: 86.8% Indels: 0
DB: 16 Gaps: 0

US-10-817-483-2 (1-239) x US-11-156-084-20 (1-723)

Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db 1 ATGATCTGGCGCTATATTTTCGCTCAACTGACAGGAAGACCTCGACCGCGGTAGCT 60
Qy 21 LeuAlaGlnIleThrGlyLeuProValLeuSerLeuAspArgValGlnCysArgProGln 40
Db 61 CTTGCCACAGACACTGGGCTTCACAGCTTCCTGCTGCATCGGAGTCCAAATTTCTCTCAG 120
Qy 41 LeuSerThnGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db 121 CTGTCAACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGGAACGAGCGGTATATC 180
Qy 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 181 CTTGATGATCGGCTCTGTGTGAAGGGTATCATCGACGCCAACAGCTCATGAAGGCTG 240
Qy 81 IleAlaGluValHisAsnHisGlnAlaLysGlyLysGlyLeuIleLeuGluGlySerIle 100
Db 241 ATGGGGGGGGGTATATATATATATAGAGCCGACGCGGCTTATTTCTGAGGAGAGATCTATC 300
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTPaAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAAGTGCATGCGCCGCAAGCAGTATTTGGAGTGGCGATTTTCTTGCGCATATT 360
Qy 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db 361 ATTCGCCACAGATTTAGCAGACGAAAGACCTTCATGAACTGGCCCAAGGCCAGAGTTAAG 420
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCTGCTGCTCAGAGCTTTCTATTTATTCAGAGTTGGTATCTTTGGAAA 480
Qy 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 481 GAGCTCGGCTGAGGCGCCACTACTGAAAGAGATCGATGATCGATATGCTCATGCTGTTGTT 540
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCAGAAACAGATCATCATCGATATGCTATGACCTTGACGCAATATGAGAGAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
Db 601 AAGTTGATTCATGGATGCTCAGAGATATCTCATTCATCATGACGCCGACAAAGACGAAA 660
Qy 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAAGCGAGCGGCTTACGACGAGATTCGAAGTTCATTCATTCGGAATG 717

RESULT 15

US-10-369-493-38969
; Sequence 38969, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38969
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-38969

Alignment Scores:

Pred. No.:	8.11e-128	Length:	720
Score:	1065.00	Matches:	205
Percent Similarity:	93.3%	Conservative:	18
Best Local Similarity:	85.8%	Mismatches:	16
Query Match:	86.7%	Indels:	0
DB:	7	Gaps:	0

US-10-817-483-2 (1-239) x US-10-369-493-38969 (1-720)

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QY      1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
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Db      1 ATGATCTGCGCTTAATTTTCGGTCCAACTTGACAGAAAGACGTGACCGCGTAGCT 60
QY      21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
      |||
Db      61 CTTGCCCGCAGACTGGGCTTCCAGTCTTCGCTCGATCCGGTCCAAATGTTGCTCCAG 120
QY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
      |||
Db      121 CTGTCAACCGAAGCGAGCGACCAACACTGGAGAAAGACTGAAAGACAGCCGCTTATAC 180
QY      61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
      |||
Db      181 CTTGATGATCGGCTCTGTGTAGAGGTATCATCCGACCAAGCAAGTCATGAAGGCTG 240
QY      81 IleAlaGluValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGluGlyGlySerIle 100
      |||
Db      241 ATGGGGGGGTGTATTAATTATGAGGCCCAAGCCGGGCTTATCTTGAGGGAGATCTATC 300
QY      101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
      |||
Db      301 TCGTTTGCTCAAGTGCATAGCGCAAGACGTTATGAGTGCAGATTTTCGTTGGATAT 360
QY      121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaLysThrArgValLys 140
      |||
Db      361 ATTCGCCACGAGTTAGACGAGAGAGACCTTCATGAACGTGGCCAAAGCCAGAGTTAAG 420
QY      141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
      |||
Db      421 CAGATGTTACCGCCCTGTGCGAGGCTTCTATTAATCCAAAGAGTTGTTGATCTTGGAAA 480
QY      161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
      |||
Db      481 GAGCTTCGCTGAGGCCCATCTAGTAAGAGATCGATGATATCGATATGCCATGTTGTTT 540
QY      181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
      |||
Db      541 GCTAGCCGACGAGACAGATCACATCCGATATGCTATGTCAGCTTGACGCGAGATATGAGGAT 600
QY      201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnLys 220
      |||
Db      601 AAGTTGATTCATGGATCGCTCAGAGATATCTCATTCATGCAACGCCGCAAGAAACAGAAA 660
QY      221 PheProLeuValGlyAlaThrAlaValAlaGlnLysGlyProProPheArgMet 239
      |||
Db      661 TTCCTCGAGTTAACGACGCCGCTTACGACGAGATTGAAAGGTATCATTCATTCGGAATG 717

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Search completed: June 26, 2006, 22:39:43
 Job time : 1283 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 20:38:53 ; Search time 38 Seconds
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2261.614 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
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Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104.5	8.5	945	US-10-471-571A-2309	Sequence 2309, Ap
2	83	6.7	2232	US-11-217-529-81083	Sequence 81083, A
3	82.5	6.7	1011	US-10-471-571A-2959	Sequence 2959, Ap
4	82.5	6.7	1501	US-10-449-902-19636	Sequence 19636, A
5	82.5	6.7	2880	US-10-449-902-19584	Sequence 19584, A
6	82	6.7	632	US-10-953-349-25636	Sequence 25636, A
7	81.5	6.6	1798	US-11-293-697-1637	Sequence 1637, Ap
8	81.5	6.6	2465	US-10-449-902-10002	Sequence 10002, A
9	81.5	6.6	2989	US-10-449-902-22349	Sequence 22349, A

10	81.5	6.6	3243	7	US-11-217-529-76988	Sequence 76988, A
11	81	6.6	651	6	US-10-488-619-1211	Sequence 1211, Ap
12	81	6.6	659	6	US-10-488-619-1209	Sequence 1209, Ap
13	81	6.6	1634	7	US-11-293-697-1892	Sequence 1892, Ap
14	80.5	6.5	1061	6	US-10-449-902-28331	Sequence 28331, A
15	80.5	6.5	2119	6	US-10-449-902-18278	Sequence 18278, A
16	80.5	6.5	2511	6	US-10-449-902-17618	Sequence 17618, A
17	80	6.5	1672	6	US-10-449-902-20437	Sequence 20437, A
18	80	6.5	2353	6	US-10-449-902-14983	Sequence 14983, A
19	79.5	6.5	1287	6	US-10-449-902-1478	Sequence 4778, Ap
20	79.5	6.5	1377	6	US-10-953-349-5460	Sequence 5460, Ap
21	79.5	6.5	1843	6	US-10-449-902-4417	Sequence 4417, Ap
22	79.5	6.5	1974	6	US-10-449-902-15620	Sequence 15620, A
23	79.5	6.5	2049	7	US-11-217-529-79820	Sequence 79820, A
24	79	6.4	3129	6	US-10-548-484-52	Sequence 52, Appl
25	79	6.4	19634	6	US-10-517-441-84	Sequence 84, Appl
26	78.5	6.4	789	6	US-10-471-571A-4555	Sequence 4555, Ap
27	78.5	6.4	1194	6	US-10-471-571A-661	Sequence 661, Appl
28	78.5	6.4	1487	6	US-10-449-902-22890	Sequence 22890, A
29	77.5	6.3	2017	6	US-10-449-902-7616	Sequence 7616, Ap
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31	77	6.3	720	7	US-11-217-529-2991	Sequence 2991, Ap
32	77	6.3	1629	6	US-10-449-902-9909	Sequence 9909, Ap
33	77	6.3	3756	6	US-10-449-902-12827	Sequence 12827, A
34	76.5	6.2	1023	7	US-11-217-529-78199	Sequence 78199, A
35	76.5	6.2	1216	6	US-10-449-902-21395	Sequence 21395, A
36	76.5	6.2	1638	7	US-11-217-529-79683	Sequence 79683, A
37	76	6.2	709	6	US-10-449-902-7541	Sequence 7541, Ap
38	76	6.2	795	7	US-11-217-529-77108	Sequence 77108, A
39	76	6.2	1392	7	US-11-217-529-516	Sequence 516, Ap
40	76	6.2	1637	6	US-10-449-902-15922	Sequence 15922, Ap
41	76	6.2	1637	6	US-10-449-902-22949	Sequence 22949, A
42	76	6.2	1723	6	US-10-449-902-8091	Sequence 8091, Ap
43	75.5	6.1	1399	6	US-10-449-902-11273	Sequence 11273, A
44	75.5	6.1	5040	7	US-11-217-529-77055	Sequence 77055, A
45	75	6.1	1011	7	US-11-217-529-80402	Sequence 80402, A

ALIGNMENTS

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US-10-471-571A-2309
; Sequence 2309, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US-10/471,571A
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqMan99, version 1.03
; SEQ ID NO 2309
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-2309

Alignment Scores:
Pred. No.: 0.0013 Length: 945
Score: 104.50 Matches: 57
Percent Similarity: 39.4% Conservative: 38
Best Local Similarity: 23.7% Mismatches: 63
Query Match: 8.5% Indels: 83
DB: Gaps: 12

US-10-817-483-2 (1-239) x US-10-471-571A-2309 (1-945)
Oy 5 LeuIlePhgIyProThCysThrcIyIyThrsrTrAlaIleAlaLeuAlaGlnIn 24
Db 40 GTAATTGGGGCCACATGCTTCAGGTAAACAGACGCTTTCAGTCGAACTCGCAGAGCT 99
```

```
Qy      25 ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrGly 44
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      100 ATCAATGATGTAATCATTAAGCGGTGACTATGACAGCTCAACAAACATATTAATTCGA 159
Qy      45 SerGlyArgProCysProValGlnGluLeuLeuGlySerGlyThrThrArgLeuTyrLeuAspArg 64
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      160 ACTGCAGAAAGTAAACCTGAAAGAAATGAGATGATTCACATCATTTAATTAATGAT----- 213
Qy      65 ProLeuVallysglylellelethrAla-----LysGln 75
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      214 -----ATCTTGAAATCCGATGATACATTTTCAGCATATGAAATTCGAAGGA 258
Qy      76 AlaHisGluArgLeuIleAlaGluValHisAsnHisGluAlaLysGlyLeu---Ile 94
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      259 TTACAGAGAAAGATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 309
Qy      95 LeuGluGlySerIleSerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAla 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      310 ATAGCAGGTGGAACAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 345
Qy      115 AspPheArgTrpHisIleIleArgAsnGluLeuAlaAspGluGluSerPheMetSerVal 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      346 -----ATATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 372
Qy      135 AlaLysThrArgValLysGlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlu 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      373 -----ACAGTTACACCT---GCACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 408
Qy      155 LeuValGlnLeuTrpArgGluProArgLeuArgProIleLeuGluGlyIleAspGlyTyr 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      409 AAGTTAATCT-----GCATTAGAACATTAGAT----- 435
Qy      175 ArgTyrAlaLeuLeuPheAlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeu 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      436 -----AATCAGCAACTACACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 468
Qy      195 AspAla---AspMetGluAsnLysLeuIleHisGlyIleAlaGlnGluPheLeuIleHis 213
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      469 GATGGGTTTCTGCAGAAAT-----ATTCACTTAAACACCGCCAAAGAGTGTGGC 522
Qy      214 Ala-----ArgArgGlnGluGlnLys 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      523 CCTATTGATATTATTATTAACAAACAAACAACTTTGAGTAATCGCAAGAAAGTCGACAA 582
Qy      221 Phe 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      583 TTT 585

RESULT 2
US-11-217-529-81083
; Sequence 81083, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81083
; LENGTH: 2232
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81083
```

```
Alignment Scores:
Pred. No.: 3.27 Length: 2232
Score: 83.00 Matches: 46
Percent Similarity: 32.5% Conservative: 29
Best Local Similarity: 19.9% Mismatches: 72
Query Match: 6.7% Indels: 84
DB: 7 Gaps: 9

US-10-817-483-2 (1-239) x US-11-217-529-81083 (1-2232)
Qy      5 LeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAlaLeuAlaGlnGln 24
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      214 CTTATGTTTCATAGCAACCATTAACAGTAAATCTAAGTGGCCGACCGATCCAAACAA 273
Qy      25 Thr----- 25
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      274 ACGGTTAACAAATATATAGCTGTGGAATTTTTTGTCTTAATAATTAATTAATTAATTAATTC 333
Qy      26 -----GlyLeuProValLeuSerLeuAsp-----ArgValGln 36
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      334 ATGACATCGATTCATCCGGTTATCCGATTTAATGATTAATGAGAGATTTTGCATTAAGC 393
Qy      37 CysCysProGlnLeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThr 56
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      394 TCGGCTCTGATATTTCACACATTTCTTATGATCATCGTTACGTTCTTCTCTCT--- 450
Qy      57 ThrArgLeuTyrLeuAspAspArgProLeuVallysglylellelethrAlaLysGlnAla 76
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      451 -----AGAGTTTGAATGCTCAAGCAACAGCT 477
Qy      77 HisGluArgLeuIleAlaGluValHisAsnHisGluAlaLysGlyLeuIleLeuGlu 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      478 CCCAAGCATTCATGCTCAAGCACTAAGAAAG-----CTTTATCA 516
Qy      97 GlyGlySerIleSerLeu-----LeuArgCysMetAlaGlnSerArg--- 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      517 AATGATCTTTTACTACAGCAGCATTTGATTTAATCTTACATGCAAAACGGGGA 576
Qy      111 -----TyrTrpAsnAlaAspPheArgTrpHis----- 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      577 TTCACGAAACACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 636
Qy      120 -----IleIleArgAsnGluLeuAla 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      637 CTTATGACGAATCATCATACAGACAGACACTAGATGTAACGCCAAAGAACTATTG 696
Qy      127 AspGluSerPheMetSerVal-----AlaLysThrArgVallysgln 141
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      697 GATCACAAGAGATTCCTACACACCGTAAATCCGAGGTTTGCTGAACAAATTTTAAGCTAT 756
Qy      142 MetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArgGlu 161
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      757 ATTAATAGGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 810
Qy      162 ProArgLeuArgProIleLeuGluGlyTyrIleAsp 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      811 GCAGGCACAGAGTTTAATGCAAGTGTATTAAT 843

RESULT 3
US-10-471-571A-2959
; Sequence 2959, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqMan99, version 1.03
```


SEQ ID NO 2959
LENGTH: 1011
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-10-471-571A-2959

Alignment Scores:
Pred. No.: 1.24 Length: 1011
Score: 82.50 Matches: 49
Percent Similarity: 36.2% Conservative: 27
Best Local Similarity: 23.3% Mismatches: 67
Query Match: 6.7% Indels: 68
DB: Gaps: 9

US-10-817-483-2 (1-239) x US-10-471-571A-2959 (1-1011)

```
QY 43 ThrGlySerGlyAArgProThrValGluGluLeuLysGlyThrThrArgLeuTyrLeuAsp 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 220 ACAAGCTGAAGGTGAGCACTGATTCGCAATTGAAAGTTACTTGCATATCTATGCAAGT 279
QY 63 AsparGProLeuValLysGlyLleIleThrAlaLysGlnAlaHisGluArgLeuIleAla 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 GATTATCGTCTGTCAGAGGTATTAAGATAAATTCAA-----ATTAG 324
QY 83 GluValHis-----AsnHisGluAla----- 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 GAAGTTCATGTTGTTCTGCGTATGCTGATTAATGATCATCTGTTAAACAGAAATTAGT 384
QY 90 ---LysGlyGlyLeuIleLeuGluGly-----GlySerIleSerLeu-Le 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 AGACAAGCGAGTCAATTACTTGAAGGCATATTACAAAGAACGCCGATGCTGTAAGT 444
QY 103 uArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTyrHisIleAlaArgAs 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 G-----GCGATTCACGATGGCATGTGTTA----- 469
QY 123 ngIuLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLysGlnMetLe 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 -----GTGAGCAATTCAT 483
QY 143 uArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGln-----Le 158
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 484 TTATTATCCATTAATGATATTCTTCGATCCAGCAGAGGTGACCTAGGCCAAATGTTGTC 543
QY 158 uTrpArgGluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLe 178
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 TTTCAGGCAACACATTGCAACGATGAGCAACAAC-GCTGGCGGTATTATACGAC 602
QY 178 uLeuPheAlaThrGlnAsn-----GlnIleThrProAs 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 603 GATGATATGATCCTGATATGTCAGTGAAACAATATATACATTGTTGTAGAGCCATC 662
QY 189 pMetLeuLeuGlnLeuAsp---AlaAspMetGluAsnLysLeuIleHisGlyIleAlaG1 208
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 663 AGTCATTAACACTTTTAGACAAATTAACACACAAACGTTATATTACAGGGAGTGGA 722
QY 208 ngIuPheLeuIleHisAlaArgArgGln 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 723 TGGCGTGAAGATGGCGCATCGACGTCAA 750
```

RESULT 4
US-10-449-902-19636

; Sequence 19636, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agricultural Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USRS THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449, 902

; CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19636
LENGTH: 1501
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK069984
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-19636

Alignment Scores:

Pred. No.: 2.15 Length: 1501
Score: 82.50 Matches: 59
Percent Similarity: 36.8% Conservative: 44
Best Local Similarity: 21.1% Mismatches: 74
Query Match: 6.7% Indels: 104
DB: Gaps: 11

US-10-817-483-2 (1-239) x US-10-449-902-19636 (1-1501)

```
QY 5 LeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAlaLeuAlaGln--- 23
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 TTGCTTTATGGGCTCCCGGCACTGGGAAACATGACAAATACCTGCGCTTCCAGGAAG 411
QY 24 -----GlnThrGly 26
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 412 TTGTATGGGTCACTATGAGCAACATGATTTCTGAATCTCATGATCAGATAGCGTGT 471
QY 27 LeuProValLeu-----SerLeuAspArgValGlnCysCysProGln-LeuSerThrG1 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 ATTGATGTTTGAAGCAGCAACAAATCCA-AGACTTCGCAAGTGGCCGCAAGTCTCTTTCGG 530
QY 44 ySerGly----- 46
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 531 AGCAAGAACATCTTGAATGATGTTCTATTGATGAGAACAGATGCCATGACCAAGATGC 590
QY 47 -----ArgProThrValGluGluLeuLysGlyThrThrArgLeuTyrLeuAs 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 591 ACAAGTTGCATTCGCAAGAGTCATTGAGAGATACAAAGAGCAACAGGTTTGGCTGAT 650
QY 62 pAspArgProLeuValLysGlyLleIleThrAlaLysGlnAla----- 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 651 ATGCACCATGTGAACAAH---ATCATTCACGACTGCAATCAAGTGCACACAGGTTAG 707
QY 77 -----HisGluArgLeuIleAlaGluValHisAsnHi 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 708 ATTGCACCCCTTGATGCACTCATGTTAGGAAAGTCTT-----AAACATATAAT 758
QY 87 sGluAlaLysGlyLeuIleLeuGluGlySerIleSerLeuLeuArgCysMetAl 107
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 759 ACAATCCAGGGCTTGATGATGATGACGGGTGTTGACAGCCCTTGCGGTAAAGT-- 816
QY 107 aGlnSerArgTyrTrpAsnAlaAspPheArg-----TrpHi 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 817 -----AATGTTGATATGAGAGAGAGGCTTTGAACATATTGCACTCAACACA 860
QY 119 sIleIleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgVa 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 861 CATGGCATCTTAAGCAATAACAGAGAGAGCTGTGATCTTGACACAGAAACCCCATGCC 920
QY 139 lLysGlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTr 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 921 GAAACACAT-----GAAACATGACATGACTG 947
QY 159 P-----ArgGluProArgLeuArgPr 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 948 GTTGTGATGATATCATTTTCAACAGCTTCAATATGATATCTGATATGAAGATGAGAA 1007
```


Oy	60	TyrLeuAspAspArgProLeuValylsGlyIleIleThrAlaIysGlnIleHisGlyArg	79
Db	100	TCTTGAATTTGGACCTCTATCTCTTATGAGACTTTGACCTTCAAAAGAAC	50
Oy	80	LeuIleAlaGluValHisAsnHisGluAlaIylsGlyIleLeuIleLeuGlu	96
Db	49	-----GTTGGCGTGAAATGAAAAACGAAACCAATGAGTCAAAATGTTGAA	5
RESULT 7			
US-11-293-697-1637			
; Sequence 1637, Application US/11293697			
; Publication No. US20060105376A1			
GENERAL INFORMATION:			
APPLICANT: HELIX RESEARCH INSTITUTE			
TITLE OF INVENTION: Novel full length cDNA			
FILE REFERENCE: HI-A0106			
CURRENT APPLICATION NUMBER: US/11/293,697			
CURRENT FILING DATE: 2005-12-05			
PRIOR APPLICATION NUMBER: US/10/108,260			
PRIOR FILING DATE: 2002-03-28			
NUMBER OF SEQ ID NOS: 5458			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 1637			
; LENGTH: 1798			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-293-697-1637			
Alignment Scores:			
Pred. No.:	3.61	Length:	1798
Score:	81.50	Matches:	54
Percent Similarity:	39.14	Conservative:	43
Best Local Similarity:	21.84	Mismatches:	82
Query Match:	6.64	Indels:	69
Db:	7	Gaps:	11
US-10-817-483-2 (1-239) x US-11-293-697-1637 (1-1798)			
Oy	21	LeuAlaGlnGlnThrArgIleu-----	ProValIleuSerLeuAsp 33
Db	659	CTTGCCCGAGAGAAATCCATAGAGAAAGATGCTCTATGAGAAACCAATTCAGAGCTGCAC	718
Oy	34	ArgValGlnCysCysProGlnIleuSerThrGlySerGlyArgProThrValGlnGluIleu	53
Db	719	AGACTTGTAG-----	CAAAACACG 736
Oy	54	LysGlyThrThrArgLeuTyrIleuAspAspArgProLeuValIysGlyIleIleThrAla	73
Db	737	AAAGAAACCTACCGCGCGCATGCTAGACGAG-----	CTGTTGCTGGCC 778
Oy	74	LysGlnAlaHisGluArgLeuIleAlaGluValHisAsnHisGluAlaIylsGly-----	91
Db	779	GAGAAAGTGTCAATAGCGCACCTATATACAGATTAGAGAAACGAGAACATTAACACACTGAC	838
Oy	92	-----GlyLeuIleLeuGlnGlyIylSerIleSerLeuIleu	103
Db	839	TACATGAACAAGAGCGACGACTTCAACCAACCTGCTGAGACGAGCGGAGAGGTTAA	898
Oy	104	ArgCysMetAlaGlnSerArgTyrTrpAsnAla-----	AspHeArg 117
Db	899	AAGCTCCCTTGAAACAAGAAAGGCTTATCAAGCCCGCAAGAAAGAAATGCTTAAACGA	958
Oy	118	TrpHisIleIleArgAsnGluLeuAlaAspGlnIleuSerPheMetSerValAlaIylsThr	137
Db	959	CTCATTAACATAAGATGATGAGCTTGTATAACTCAATCTTT---GCACATACGTCTGGG	1015
Oy	138	ArgValIylsGlnMetLeuArgProSerAlaGlyLeuSerIle-----IleGlnGluIleu	155
Db	1016	GATGAAGAACAAATACACATGTGAACAACCTGGCTGCAAGCCAGAAAGTACAGGATCTT	1075
Oy	156	ValGlnIleuTPrArg-----GluProArgLeuArgProIleLeuGlnGlyIleAspGly	173

Db	1076	ACTGAGAAGCTGAGGGAAGAAAGAGAGCTCAAAAGCATT-----	11117
Qy	174	TyAATgTgTAlaLeuLeuPheAlaThGlnAsnGlnIleThrProAspMetLeuLeuGln	193
Db	1118	-----ACCTCCAAATCCCAAMAGACAGACAGAAATTGCTCAGG	1156
Qy	194	LeuAspAlaAspMetGluAsnLysLeuIleHisIsgLYTLeaGlnGluPheLeuIleHis	213
Db	1157	TTAAAGTGGACCTTGGAAACAGACAGCTTCGAGCTTTCTCAAGAGCATGAAGAGATGAAC	1216
Qy	214	AlaArgArgGlnGlnGln-----LysPheProLeuValGlyAla	226
Db	1217	GCTAACTGGCTATCAAGAGTCTCAGATATAGCAACTTATGACTCAAGCTGCTGGCTTA	1276
Qy	227	Thr---AlaValGluAlaPheGlu	233
Db	1277	ACCCAAAGAAATCGAGAGCTAGAA	1300
RESULT 8			
US-10-449-902-10002			
Sequence 10002, Application US/10449902			
Publication No. US20060123505A1			
GENERAL INFORMATION:			
APPLICANT: National Institute of Agrobiological Sciences.			
APPLICANT: The Institute of Technology Research Advancement Institution.			
APPLICANT: Foundation for Advancement of International Science.			
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF			
FILE REFERENCE: MOA-A0205Y1-US			
CURRENT APPLICATION NUMBER: US/10/449, 902			
PRIOR FILING DATE: 2003-05-29			
PRIOR APPLICATION NUMBER: JP 2002-203369			
PRIOR FILING DATE: 2002-05-30			
PRIOR APPLICATION NUMBER: JP 2002-383870			
PRIOR FILING DATE: 2002-12-11			
NUMBER OF SEQ ID NOS: 56791			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 10002			
LENGTH: 2465			
TYPE: DNA			
ORGANISM: Oryza sativa			
PUBLICATION INFORMATION:			
DATABASE ACCESSION NUMBER: AK107350			
DATE: 2002-08-28			
US-10-449-902-10002			
Alignment Scores:			
Pred. No.:	5.61	Length:	2465
Score:	81.50	Matches:	41
Percent Similarity:	34.1%	Conservative:	17
Best Local Similarity:	24.1%	Mismatches:	38
Query Match:	6.6%	Indels:	75
DB:	6	Gaps:	6
US-10-817-483-2 (1-239) x US-10-449-902-10002 (1-2465)			
Qy	5	LeuIlePheGlyProThrCysThnGlyLysThnSerThrAlaIleAlaLeuAlaGlnGln	24
Db	1740	TTGTTGTTCCGGGCGGAGGAGGAGGAGCAATGCTGCAGAAAGCTATAGCCAAATGAC	1799
Qy	25	ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThnGly	44
Db	1800	GCTGGTGG--CCAGCTTCATCAATGCTCTGA-----GTCACCATCATCAATCGAAGTGT	1851
Qy	45	SerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyTLeuAspAspArg	64
Db	1852	TCGGGGAGG-----	1860
Qy	65	ProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeuIleAlaGluVal	84
Db	1861	-----ACGAGAAAAACGTC-----	1875
Qy	85	HisAsnHisGluAlaLysGlyGlyLeuIleLeuGlnGluTyGlySerIleSerLeuLeuArg	104

```
Db 1876 -----GAGCATGTCAGTTGGCTGCTAGG 1902
Qy 105 CysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIleIle----- 121
Db 1903 TTGCTCCTACATCATTTTGTG-----ATGAGGTGACAGTATGTAGACAGC 1953
Qy 122 -----ArgAsnGluLeuAlaAspGluGluSer 130
Db 1954 GCGCTCGATGCGGTGAACATGAGCGGATGCGGAAGATCAAGAAATGATTGATGAGTCACT 2013
Qy 131 PheMetSerValAlaIleThrArgValIleGln----- 141
Db 2014 GGGATGGTCTCCTGCAAAATCGGGTGAAGAAATCCTTGTCTTGCTGCTACAAATAGAC 2073
Qy 142 -----MetLeuArgProSerAlaGly 148
Db 2074 CCTTGAATCTTGATGAAGCCATCATTTAGGA 2103

RESULT 9
US-10-449-902-22349
; Sequence 22349, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22349
; LENGTH: 2989
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK072537
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-22349

Alignment Scores:
Pred. No.: 7.34 Length: 2989
Score: 81.50 Matches: 41
Percent Similarity: 34.1% Conservative: 17
Best Local Similarity: 24.1% Mismatches: 38
Query Match: 6.6% Indels: 75
DB: Gaps: 6

US-10-817-483-2 (1-239) x US-10-449-902-22349 (1-2989)
Qy 5 LeuIlePheGlyProThrCysThrGlyysThrSerThrAlaIleAlaLeuAlaGln 24
Db 1741 TTGTTGTTGGGGCCACCGGAAACAGGGAAGCAATGCTTGCAAGGCTATAGCCAAATGAC 1800
Qy 25 ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrGly 44
Db 1801 GCTGGTG--CCAGCTTCATCAATGCTCTGA-----TTCACCATCATCATGAGAGTGGT 1852
Qy 45 SerGlyArgProThrValGluGluLeuLeuysGlyThrThrArgLeuTyLeuAspArg 64
Db 1853 TCGGGGAG----- 1861
Qy 65 ProLeuValIysGlyIleIleThrAlaIysGlnAlaHisGluArgLeuIleAlaGluVal 84
Db 1862 -----ACGAGAAAACGTCC----- 1876
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Qy 85 HisAsnHisGluAlaIysGlyGlyLeuIleLeuGluGlySerIleSerLeuLeuArg 104
Db 1877 -----GAGCATGTCAGTTGGCTGCTAGG 1903
Qy 105 CysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIleIle----- 121
Db 1904 TTGCTCCTACATCATTTTGTG-----ATGAGGTGACAGTATGTAGACAGC 1954
Qy 122 -----ArgAsnGluLeuAlaAspGluGluSer 130
Db 1955 GCGCTCGATGCGGTGAACATGAGCGGATGCGGAAGATCAAGAAATGATTGATGAGTCACT 2014
Qy 131 PheMetSerValAlaIleThrArgValIleGln----- 141
Db 2015 GGGATGGTCTCATGCAAAATCGGGTGAAGAAATCCTTGTCTTGCTGCTACAAATAGAC 2074
Qy 142 -----MetLeuArgProSerAlaGly 148
Db 2075 CCTTGAATCTTGATGAAGCCATCATTTAGGA 2104

RESULT 10
US-11-217-529-76988
; Sequence 76988, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217, 529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76988
; LENGTH: 3243
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-76988

Alignment Scores:
Pred. No.: 8.22 Length: 3243
Score: 81.50 Matches: 26
Percent Similarity: 41.3% Conservative: 12
Best Local Similarity: 28.3% Mismatches: 43
Query Match: 6.6% Indels: 11
DB: Gaps: 2

US-10-817-483-2 (1-239) x US-11-217-529-76988 (1-3243)
Qy 55 GlyThrThrArgLeuTyLeuAspAspArgProLeuValIysGlyIleIleThrAlaIys 74
Db 166 GGTACAGGCGACCGCTATATATGACGATCGCCACATGTTAAACAATGCAAGTACGGGA 225
Qy 75 GlnAlaHisGluArgLeuIleAlaGluValHisAsnHisGluAlaIysGlyLeuIle 94
Db 226 CAGTACTAT-----GCTACTAACAAACAGCCAAAGCGCCCATATGTATA 267
Qy 95 LeuGluGlyGlySerIleSerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAla 114
Db 268 AATAAGAAATGTGACATCAGTAGTCGGAGGCGCATGCTCATCATCAGGTATTCAAATAGC 327
Qy 115 AspPheArgTrpHisIleIleArgAsnGluLeuAlaAspGluGluSerPheMetSerVal 134
Db 328 AAT-----GTTCACAAATACATTAGCGTCTTGAGTGAATGATCTCTTCCACA 372
Qy 135 AlaIysThrArgValIysGlnMetLeuArgProSer 146
```

DB 373 GAATCTGCTTCCTTTTGGACAAGACCACTTCA 408

RESULT 11

US-10-488-619-1211

Sequence 1211, Application US/10488619

Publication No. US20060099578A1

GENERAL INFORMATION:

APPLICANT: Greenlee, Winner and Sullivan, P.C.

TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations

FILE REFERENCE: 98-01 WO

CURRENT APPLICATION NUMBER: US/10/488, 619

CURRENT FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 3040

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1211

LENGTH: 651

TYPE: DNA

ORGANISM: Mus musculus

US-10-488-619-1211

Alignment Scores:

Pred. No.:	1	Length:	651
Score:	81.00	Matches:	31
Percent Similarity:	41.2%	Conservative:	18
Best Local Similarity:	26.1%	Mismatches:	49
Query Match:	6	Indels:	21
DB:	6	Gaps:	3

US-10-817-483-2 (1-239) x US-10-488-619-1211 (1-651)

QY 5 LeuilepneglypProthCysThrglyLysThrserThraAlaIleAlaLeuAlaGlnGln 24

DB 54 CTGCTCTGAGACCCCGACGACCTGGGAAGACATTGTTGGCCCGCTGTGCTCATCAT 113

QY 25 ThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGlnIleuSerThrgly 44

DB 114 ACAGACTGACTCTTATTTCGTGTC----- 137

QY 45 SerGlyArgProThraValGlnGlnIleuLysGlyThrThraArgLeuTyrlleuAspArg 64

DB 138 TCTGCTCTGAACTGTGACAGAAATTCATCGG-----GAAGGGCA 179

QY 65 ProLeuValLysGlyIleleThraAlaLysGlnAlaHisGlyArgLeuIleAlaGluVal 84

DB 180 AGAATGTGAGGAGCTGTTGTCTATGCGCCGAGAACTGCTCCATCATCATCTTCATG 239

QY 85 HisaenHisGlnAlaLysGlyGlyLeuIleuGlnGlyLysSer-IleSerLeuLeuArg 104

DB 240 GACGAGATTGACTTATTGCTCTCCACGCGCTGGAGGGGGCTCTGGAGGCGACAGTGAG 299

QY 104 GCysMeclAaGlnSerArgTyrrTPAsnAlaAspPheArgTrpHisIleleArg 122

DB 300 GTACAGCGCA-----CGATGCTGGAACCTGCATCATCATGAGCTTGAGG 348

RESULT 12

US-10-488-619-1209

Sequence 1209, Application US/10488619

Publication No. US20060099578A1

GENERAL INFORMATION:

APPLICANT: Greenlee, Winner and Sullivan, P.C.

TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations

FILE REFERENCE: 98-01 WO

CURRENT APPLICATION NUMBER: US/10/488, 619

CURRENT FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 3040

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1209

LENGTH: 659

TYPE: DNA

ORGANISM: Mus musculus

US-10-488-619-1209

Alignment Scores:

Pred. No.:	1.02	Length:	659
Score:	81.00	Matches:	31
Percent Similarity:	41.2%	Conservative:	18
Best Local Similarity:	26.1%	Mismatches:	49
Query Match:	6	Indels:	21
DB:	6	Gaps:	3

US-10-817-483-2 (1-239) x US-10-488-619-1209 (1-659)

QY 5 LeuilepneglypProthCysThrglyLysThrserThraAlaIleAlaLeuAlaGlnGln 24

DB 54 CTGCTCTGAGACCCCGACGACCTGGGAAGACATTGTTGGCCCGCTGTGCTCATCAT 113

QY 25 ThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGlnIleuSerThrgly 44

DB 114 ACAGACTGACTCTTATTTCGTGTC----- 137

QY 45 SerGlyArgProThraValGlnGlnIleuLysGlyThrThraArgLeuTyrlleuAspArg 64

DB 138 TCTGCTCTGAACTGTGACAGAAATTCATCGG-----GAAGGGCA 179

QY 65 ProLeuValLysGlyIleleThraAlaLysGlnAlaHisGlyArgLeuIleAlaGluVal 84

DB 180 AGAATGTGAGGAGCTGTTGTCTATGCGCCGAGAACTGCTCCATCATCATCTTCATG 239

QY 85 HisaenHisGlnAlaLysGlyGlyLeuIleuGlnGlyLysSer-IleSerLeuLeuArg 104

DB 240 GACGAGATTGACTTATTGCTCTCCACGCGCTGGAGGGGGCTCTGGAGGCGACAGTGAG 299

QY 104 GCysMeclAaGlnSerArgTyrrTPAsnAlaAspPheArgTrpHisIleleArg 122

DB 300 GTACAGCGCA-----CGATGCTGGAACCTGCATCATCATGAGCTTGAGG 348

RESULT 13

US-11-293-697-1892

Sequence 1892, Application US/11293697

Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: Novel full length cDNA

FILE REFERENCE: HI-A0106

CURRENT APPLICATION NUMBER: US/11/293, 697

CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1892

LENGTH: 1634

TYPE: DNA

ORGANISM: Homo sapiens

US-11-293-697-1892

Alignment Scores:

Pred. No.:	3.62	Length:	1634
Score:	81.00	Matches:	55
Percent Similarity:	36.5%	Conservative:	44
Best Local Similarity:	20.3%	Mismatches:	96
Query Match:	7	Indels:	76
DB:	7	Gaps:	10

US-10-817-483-2 (1-239) x US-11-293-697-1892 (1-1634)

QY 5 LeuilepneglypProthCysThrglyLysThrserThraAlaIleAlaLeuAlaGlnGln 24

DB 834 CTGATGTTGAGACCCCGACGACCTGGTAACCTATGCTAGCTAAAGCTGTTGCCACTGAA 893

QY 25 ThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGlnIleuSerThrgly 44

DB 894 TGTGTACACATCTTCAACGTTTCG-----CCTTACACTGACACT 938

Qy	45	SerGIlythrProthInValGlnGluLeu-----Lys	54
Db	939	AAATACAGAGAGTGAATCTGAGAAAGTTAGTTCGTCTGTTTGAGATGGCTAGATTTAT	998
Qy	55	GlyThrThraGleuTyrlLeuAspArgProLeuVal-----LysGlyIleIle	71
Db	999	GCCCCCTACAGATCTTCATTGATGAGTAATCTATCTTCAGTCGAAGAGAACTCT	1058
Qy	72	ThrIalysGlnIaHisGluArgLeuIleIaGlu---ValIHisGlnIaIalys	90
Db	1059	GATGAACATGGAGCAAGTCGAGAGGTCAAGTCTGAAGTCACTGATTCATTCAGATGGATGAGTT	1118
Qy	91	GlyGlyLeuIleLeuGlnGlyGlySerIleSerLeuArgCysMetAlaGlnSerArg	110
Db	1119	GGAGGAGCTTTAGAAAATATGATGATCCCTCCAAAATGTTATGATTTGGCTGTACT---	1175
Qy	111	TyrTrpAsnIaAspRheArgTrpHisIleIleArgAsnGluLeuAlaAspGlnGlnSer	130
Db	1176	-----AATTTCCCGTGGGCACTT-----GATGAAGCT	1202
Qy	131	PheMetSerValAlaIalysThraArgValIysGlnMetLeuArgProSerAlaGly-----	148
Db	1203	TTGGGAGAGAGATTAGAAAAGATATATATATACCTCTCCACAGCAAAAAGAAAGACT	1265
Qy	149	-----LeuSerIleIleGlnGluLeuValGlnLeuTrpArgGluProArgLeuArgPro	166
Db	1263	GAGCTTCTGAAAGATCAACCTTCGTGAGGTGCATATTAAGATCCGTATTAACACTGGAGAT	1322
Qy	167	IleLeuGlnGlyIleAspGlyTyr-----ArgTyrAla	177
Db	1323	ATAGCCGAGAAAGATTGAGGCTATTTCTGTCGTCTGACATCACTAATGTTTGACAGGAGATGC	1382
Qy	178	LeuLeuPheAlaTrpGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAsp	197
Db	1383	TCTTTAATGCAATGACGAGCGCGT-----	1408
Qy	198	MetGluAsnIysLeuIleHisGlyTyrLeaGlnGluPheLeuIleHisAlaArgArgGln	217
Db	1407	-----ATCAATGGCTTAAGTCCAGAGAAATCCGTGACCTTTTAAGAG	1451
Qy	218	GluGlnIysPheProLeu-----	223
Db	1452	GAACTTCAGATGCCCTGTACCAAGAGAGACTTTGAATTGGCCCTAAAGAAAATTGCTAAG	1511
Qy	224	---ValGlyAlaIatnAlaValaGluAlaPheGlu	233
Db	1512	TCTGCTCTCTGCGACGACTTGAGAAAGTATGAA	1544
<p>RESULT 14</p> <p>US-10-449-902-28331</p> <p>Sequence 28331, Application US/10449902</p> <p>Publication No. US20060123505A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: National Institute of Agrobiological Sciences.</p> <p>APPLICANT: Bio-oriented Technology Research Advancement Institution.</p> <p>APPLICANT: The Institute of Physical and Chemical Research.</p> <p>TITLE OF INVENTION: Full-length Plant cDNA and Uses Thereof</p> <p>FILE REFERENCE: MOA-A020571-US</p> <p>CURRENT APPLICATION NUMBER: US/10/449,902</p> <p>CURRENT FILING DATE: 2003-05-29</p> <p>PRIOR APPLICATION NUMBER: JP 2002-203269</p> <p>PRIOR FILING DATE: 2002-05-30</p> <p>PRIOR APPLICATION NUMBER: JP 2002-383870</p> <p>PRIOR FILING DATE: 2002-12-11</p> <p>NUMBER OF SEQ ID NOS: 56791</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 28331</p> <p>LENGTH: 1061</p> <p>TYPE: DNA</p> <p>ORGANISM: Oryza sativa</p> <p>PUBLICATION INFORMATION:</p> <p>DATABASE ACCESSION NUMBER: AK103773</p>			

; DATABASE ENTRY DATE: 2002-08-28			
; US-10-449-902-28331			
Alignment Scores:	2.26	Length:	1061
Pred. No.:	80.50	Matches:	53
Score:	37.7%	Conservative:	40
Percent Similarity:	21.5%	Mismatches:	92
Best Local Similarity:	6.5%	Indels:	63
Query Match:	6	Gaps:	11
DB:			
US-10-817-483-2 (1-239) x US-10-449-902-28331 (1-1061)			
Qy	7	PhegIyProThrCysThrGlyLeuThSerTherAlaIleAa	25
Db	54	TTCCCTCGGTGCGCGCCCTCCCGCTTCACTCATCGCAGCTTGAGCATCAAGC	113
Qy	26	GlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrGlySer	45
Db	114	GGCGGAGTGGCTCGGC--AGCGGCAGGAGTGACTCGCGCGCGGTGCTGCTTC	170
Qy	46	GlyArgProThrValGlnGluLeuLeuGlySerThrArgLeuThyTyrLeuAspAspArg	64
Db	171	GGTGGCCCTCTCTCTCTCTCTCCCTCCACGCCGCAGAGGCATGTGAATGGCGGCGCTC	230
Qy	65	---ProLeuValGlyGlyLe-1IethrAlaGlnAlaHisGlnArgLeuIleAaG1	83
Db	231	GTGCAGCATCATGGCGGATCGCGCCATCAAGTGGCTGTATCTGGGTTGTTCTTGG	290
Qy	83	ValHisAsnHisGlnAlaGlyGlyGlyLeuIleLeuGlnGlyGlySerIleSerLeu	103
Db	291	TTCTCCAC-----GCCACGGGCAACTCTCG-----	315
Qy	103	uArgCysMetalArgInserArgTyrTTPAsnAlaAspPheArgTrpHisIleIleArgAs	123
Db	316	-----CAGTCATGGCGGCCCTGCATCCGCAC-CGTGCTTCGGGAT	355
Qy	123	ngIuLeuAlaAspGlnGluSerPheMetSerValAlaLeuThrArgValGlnMetLe	143
Db	356	CCAGTGTGG-----GCTGTGCTAGGGCGCGAGCTCTCTCCAGAT	397
Qy	143	uArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArgGluProAr	163
Db	398	TGGC-----TCAGGGCCCTCGATGTGACGGCATGGGTGAGCTGTGTCAACGCGAA	451
Qy	163	GleuAspPro-----IleLe	168
Db	452	GCCTTCCCTTCGTGCGAGCAGATCGTTGTAGCGCGCGCTTCGTGAGGAGGATCAT	511
Qy	168	uGlnGlyIleAsp-----GlyTyrArgTyrAlaLeuLeuPheAlaThrGlnAsnG1	185
Db	512	TGCTTTATCGATCGATGTTCAAGTTGATGGCAATATGTTCTTATTTTGTGTTTACTGGATCA	571
Qy	185	nIle-----ThrProAspMetLeuGlnLeuAspAlaAspMetGluAs	200
Db	572	GCTGGGCTCAAGTAGCGGTACTGAGAGGTGTGATGTCCTTGATATGTGATCTTCAGAA	631
Qy	200	hysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnGly	220
Db	632	CAAGCTGATCGACAGCTTATCA-----AGGAAACCCCAAG	667
Qy	220	sPheProLeuValGlyAla	226
Db	668	ATTTGACACTGGCGGTGCA	686
RESULT 15			
US-10-449-902-18278			
; Sequence 18278, Application US/10449902			
; Publication No. US20060123505A1			
; GENERAL INFORMATION:			
; APPLICANT: National Institute of Agrobiological Sciences.			
; APPLICANT: Bio-oriented Technology Research Advancement Institution.			
; APPLICANT: The Institute of Physical and Chemical Research.			

; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 18278
 ; LENGTH: 2119
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: AK068682
 ; DATABASE ENTRY DATE: 2001-12-06
 ; US-10-449-902-18278

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
5.94	80.50	2119	71
Percent Similarity:	38.44%	Conservative:	47
Best Local Similarity:	23.1%	Mismatches:	101
Query Match:	6.5%	Indels:	89
DB:	6	Gaps:	14

US-10-817-483-2 (1-239) x US-10-449-902-18278 (1-2119)

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QY      13 GlyLysThrSerThraIleAlaIleuAlaGlnGlnThrGlyLeuProValLeuSerLeu 32
DB      379 GGACCAAGATCCGGGCGCTCAACGCTCGGCGAGACTGCCCGCTCTCGACCG 438
QY      33 AsparGValGlnCysCysProGlnLeuSerThrGlySerGlyArg----- 47
DB      439 CCT--CTACAGCTTCTGCGACACCTACCGCGGGGATCCGTGCGGCGCCGCTCAAGCT 495
QY      48 -----ProThrValGlnGlnLeu 53
DB      496 CAACACGCGGCACGACATCGCATCACTGGGCGGCGGCTCCACACGACGAGAAATG 555
QY      54 LysGlyThrThrArgLeu-TyrLeuAspAspArgProLeuValLysGlyIleIleThrAl 73
DB      556 CGAGGCGCTCGGAGATTCTGCTACGCAACGAC-----ATCGTCTCGCCCATCTCGAGCT 609
QY      73 alyseGlnAlaHisGluArgLeuIle-----AlaGluValHisAsnHisGluAlaLys 90
DB      610 CCTCAAAATACCAACAGCGTGTCTCTATGTGATATCGATATCCACCATGGGAGATGTGT 669
QY      90 sGlyGlyLeuIleLeuGlnGly-----GlySerIleSerLeuLeuArgCysMet----- 106
DB      670 -GGAAGAGCGCTTTCACACGACGACGACGATGACGCTCGTTCACAAAGTTTGGGG 728
QY      107 -----AlaGlnSerArgTyrTyr-AsnAlaAspPheArgTyrPheIst 120
DB      729 ATTATTTCCCGGGGACCGGGGACATTCGCGATATTGGGCATCAAGGGGAAGTATTACT 788
QY      120 IeIleArgAsnGlnLeu-----AlaAspGlnGluSerPheMetSerValAlaLysT 137
DB      789 CTCTGAATGTCCTCGTTGACGACGCGATATGACGACGAGCTACCACTGTTGTTCAAGC 848
QY      137 hr-----ArgValLysGlnMetLeuArgProSerAla----- 147
DB      849 CGATCATGGGGAAGGATGAGAGTTCCTGCGCCCTGCGCGGATGCTCCAGTGGCGTG 908
QY      148 -----GlyLeuSerIle-----IleGlnG 154
DB      909 CGGACTCTCTCGGGGTAGATTGGGTGCTTCAACTGCAATCAGGGGCCACGCGG 968
QY      154 IuLeuValGlnLeuThrPargLupProArgLeuArgProIleLeuGlnGlyIleAspGlyT 174
DB      969 AATGCGTAGATTCAATGAGGCTCTTCATATGCCGCTGTGCTGCTGGTGGTGGGT 1028
  
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QY      174 YrArg-----TyrAlaLeuLeuPheAlaThrGlnAsnG 185
DB      1029 ATACCATTAAGAAATGTTCGCGCGTGTGGTGTCTATGACAGAGAGTTGCATTTGATCAG 1088
QY      185 IuIleThr-----ProAspMetLeuIst 192
DB      1089 AGCTCACTGACAAAGATGCTCCAAATGAGTATTTGAGTACTTTGGTCCAGATTTATACAC 1148
QY      192 eugGlnLeu---AspAlaAspMetGluAsnLysLeuIleHisGlyIleAlaGlnGluPheI 211
DB      1149 TTCATGCTTGACACCAAGTAAATGAGAGAAACAAAACACACGCGACGAGTTGATGAT----- 1204
QY      211 euIleHisAlaArgArgGlnGlnGlnLysPheProLeuValGlyAlaThrAlaValGluA 231
DB      1205 --ATAAGATCAAGACTTCTTGATTAATCTTTCAAACTTCGACATGCTCCTAGCTTCAAT 1262
QY      231 IaPheGlnGlyProPro 236
DB      1263 TTCAAGGCGACCCCT 1279
  
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Search completed: June 26, 2006, 20:40:50
 Job time : 45 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1919	100.0	1919	2	C0895587	C0895587 Sequence
2	1919	100.0	1919	15	ABRTIPT	X14410 Agrobacteri
3	1104.8	57.6	206479	15	AB016260	AB016260 Agrobacte
4	1093.8	57.0	9931	15	AE007927	AE007927 Agrobacte
5	1093.8	57.0	10377	15	AE009419	AE009419 Agrobacte
6	1089.8	56.8	1997	15	AB025109	AB025109 Agrobacte
7	1060.8	55.3	29524	15	ATU23758	A1237588 Agrobacte
8	976.6	50.9	1983	15	ATTMPRT1	X00639 Agrobacte
9	958.4	49.9	2455	2	BD016312	X00639 Agrobacte
10	958.4	49.9	2455	2	E00404	BD016312 Method of
11	958.4	49.9	2455	2	E00404	E00404 T1 plasmid
12	958.4	49.9	2455	2	AE0046	E00404 DNA fragmen
13	958.4	49.9	2455	2	AR364803	AR364803 Sequence
14	958.4	49.9	2455	15	ATACHS	X00493 Agrobacteri
15	958.4	49.9	19410	15	AF242881	AF242881 Agrobacte
16	958.6	47.3	2724	15	AE032122	X00010 Agrobacteri
17	897	45.7	6482	15	AVIAM	AB031222 Agrobacte
18	877.8	45.7	14960	15	AVU83986	X77357 A.vitis laa
						U83986 Agrobacteri

C	34	252	13.1	1339	15	ATTU19150
C	35	231.2	12.0	584	2	I184939
C	36	216	11.3	3271	15	IS41PIVY
C	37	203.8	10.6	4679	15	ATP1DNA
C	38	198.2	10.3	813	15	ARTSG
C	39	194.6	10.1	4660	15	AB025110
C	40	190.6	9.9	1413	15	ATVTS
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C	35	231.2	12.0	584	2	I184939
C	36	216	11.3	3271	15	IS41PIVY
C	37	203.8	10.6	4679	15	ATP1DNA
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C	40	190.6	9.9	1413	15	ATVTS
C	41	190.6	9.9	206479	15	AB016260
C	42	189	9.8	1403	2	I05195
C	43	189	9.8	1403	15	ATTGSI
C	44	189	9.8	2171	15	AE007942
C	45	189	9.8	10165	15	AE009435

ALIGNMENTS

RESULT	1
LOCUS	CO895587
DEFINITION	Sequence 1 from Patent WO2004090143.
ACCESSION	CO895587
VERSION	CO895587.1 GI:55467720
KEYWORDS	
SOURCE	
ORGANISM	Agrobacterium tumefaciens (Rhizobium radiobacter)
	Agrobacterium tumefaciens
	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
	Rhizobiaceae; Agrobacterium.
REFERENCE	1
AUTHORS	Habben,J.E., Zinselmeier,C., Tomes,D.T., Abbitt,S.E., Helentjaris,T.G. and Niu,X. Modulation of cytokinin activity in plants Patent: WO 2004090143-A, 1 21-OCT-2004; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers
TITLE	
JOURNAL	
FEATURES	

FEATURES

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ORIGIN

Query Match	100.0%;	Score 1919;	DB 2;	Length 1919;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1919; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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RESULT 2
ABTIPT 1919 bp DNA linear BCT 12-SEP-1993
LOCUS Agrobacterium tumefaciens Ti plasmid ipt gene for isopentenyl
DEFINITION transferase.
ACCESSION X14410 X17432
VERSION X14410.1 GI:38689
KEYWORDS ipt gene; isopentenyl transferase; transferase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 1919)
AUTHORS Strabala,T.U., Bednarek,S.Y., Bertoni,G. and Amasino,R.M.
TITLE Isolation and characterization of an ipt gene from the Ti plasmid
B0542
JOURNAL Mol. Gen. Genet. 216 (2-3), 388-394 (1989)
PUBMED 2747621
REFERENCE 2 (bases 1 to 1919)

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RESULT 3			
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LOCUS	ABO16260	206479 bp DNA circular BCT 24-JAN-2004	
DEFINITION	Agrobacterium tumefaciens plasmid pTi-SAKURA, complete sequence.		
ACCESSION	ABO16260	AB006857 AB006858 AB007145 AB007188	
VERSION	ABO16260.1	GI:6498173	
KEYWORDS	.		
SOURCE	Agrobacterium tumefaciens (Rhizobium radiobacter)		
ORGANISM	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.		
REFERENCE	1	Hattori,Y., Suzuki,K., Uraji,M., Ohta,N., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (I): strategy for DNA sequencing of a Japanese cherry-Ti plasmid Nucleic Acids Symp. Ser. 37, 159-160 (1997) 9586048	gene CDS
JOURNAL PUBMED	2	Hattori,Y., Suzuki,K., Ohta,N., Uraji,M., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (V): Complete nucleotide sequence of plasmid pTi-SAKURA's vir region in Agrobacterium tumefaciens Nucleic Acids Symp. Ser. 39, 265-266 (1998) 954202	gene CDS
JOURNAL REFERENCE	3	Ohta,N., Suzuki,K., Hattori,Y., Uraji,M., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (III): Characteristics of T-DNA Nucleic Acids Symp. Ser. 39, 185-186 (1998)	gene CDS
JOURNAL TITLE	4	Uraji,M., Suzuki,K., Ohta,N., Hattori,Y., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (IV): Characteristics of tra region Nucleic Acids Symp. Ser. 39, 187-188 (1998)	gene CDS
JOURNAL REFERENCE	5	Suzuki,K., Ohta,N., Hattori,Y., Uraji,M., Kato,A. and Yoshida,K. Novel structural difference between nopaline- and octopine-type trb genes: construction of genetic and physical map and sequencing of trb/trai and rep gene clusters of a new Ti plasmid pTi-SAKURA Biochim. Biophys. Acta 1396 (1), 1-7 (1998) 954202	gene CDS
JOURNAL PUBMED	6	Suzuki,K., Hattori,Y., Uraji,M., Ohta,N., Iwata,K., Murata,K., Kato,A. and Yoshida,K. Complete nucleotide sequence of a plant tumor-inducing Ti plasmid Gene 242 (1-2), 331-336 (2000) 10721727	gene CDS
JOURNAL TITLE	7	(bases 1 to 206479) Suzuki,K. and Yoshida,K. Direct Submission Submitted (22-JUL-1998) Kazuo Yoshida, Hiroshima University, Faculty of Science, Kagamiyama 1-3-1, Higashihiroshima-shi, Hiroshima 739, Japan (E-mail:kazuoki@ipc.hiroshima-u.ac.jp, Tel:0824-24-7456, Fax:0824-24-0733) On or before May 14, 2001 this sequence version replaced gi:2982699, gi:2982703.	gene CDS
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57.6%; Score 1104.8; DB 15; Length 206479;

Best Local Similarity 85.5%; Pred. No. 0;
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RESULT 4
AE007927 9931 bp DNA linear BCT 28-MAY-2004
LOCUS Agrobacterium tumefaciens str. C58 plasmid Ti, section 5 of 20 of
DEFINITION the complete sequence.
ACCESSION AE007927 AE007871
VERSION AE007927.2 GI:16271969
KEYWORDS
SOURCE Agrobacterium tumefaciens str. C58
ORGANISM Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE
AUTHORS Hinkle,G., Slater,S.C. and Goodner,B.
TITLE Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
Disease in Plants
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9931)
AUTHORS Hinkle,G., Slater,S.C. and Goodner,B.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
Cambridge, MA 02139, USA
COMMENT On Oct 19, 2001 this sequence version replaced gi:15163470.
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LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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Agrobacterium tumefaciens str. C58 Ti plasmid, section 2 of 21 of
the complete sequence.
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Agrobacterium tumefaciens str. C58
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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1 (bases 1 to 10377)
Wood, D.W., Secudai, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,
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TITLE Zhao Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V. and Nester, E.W.
The genome of the natural genetic engineer Agrobacterium tumefaciens C58
JOURNAL Science 294 (5550), 2317-2323 (2001)
PUBMED 11743193
REFERENCE 2 (bases 1 to 10377)
AUTHORS Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida, N.F., Jr., Zhou, Y., Boyee, D., Sr., Chapman, P., Clendenning, J., Deatherage, G., Gillet, M., Grant, C., Guenther, D., Kutayavin, T., Levy, R., Li, M., McClelland, E., Palmeri, A., Raymond, C., Rouse, G., Saenphimachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, J., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon-Kamm, B., Liao, L., Kim, S., Hendrick, C., Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V. and Nester, E.W.

TITLE Direct Submission
JOURNAL Submitted (27-SEP-2001) Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA 98195-7242, USA
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RESULT 6
AB025109 1997 bp DNA linear BCT 27-MAR-1999
LOCUS Agrobacterium tumefaciens gene for isopenentenyl transferase,
DEFINITION complete cds.
ACCESSION AB025109
VERSION AB025109.1 GI:4586309
KEYWORDS isopenentenyl transferase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 1997)
Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawakita,A. and
Moriwae,N.
TITLE Agrobacterium tumefaciens plasmid pO22 isopenentenyl transferase (ipt)
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 1997)
Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawakita,A. and
Moriwae,N.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Takehide Kasahara, Nippon Paper Industries

Co., Ltd. R&D Div., Wood Bio-engineering Central Research Lab.:
5-21-1, Oji, Kita-ku, Tokyo 114-0002, Japan
(E-mail: takek@mtj.biglobe.ne.jp, Tel: 81-3-3911-5106 (ex. 292),
Fax: 81-3-3914-3350)

FEATURES

source

1. 1997

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688. 1410

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ORIGIN

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Matches 1270; Conservative 0; Mismatches 212; Indels 13; Gaps 4;

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DB 121 TTGAAGTTGCAATTAATGAT-----GTAATAGTAATAATTAATCACTGTGCAATTA 174
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DB 175 GAAATGGACCTGTATTTCAACCATATCTTGTATCTGTGACAAATGACACGATCGACG 234
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DB 1434 CTGCTTCATTTGAATTAAGATGTTGCAATGTTTGAAGCTTGTCTTGTGTGTGG 1488

RESULT 7
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LOCUS Agrobacterium tumefaciens Ti plasmid pTiC58 T-DNA region.
DEFINITION AJ237588
ACCESSION AJ237588
VERSION AJ237588.1 GI:5042179
KEYWORDS acrocinopine synthase; agrocinopine synthase; IAH; isopenentenyl transferase; nopalline synthase; ornithine cyclodeaminase; protein 6a; protein 6b; torf1 gene; torf10 gene; torf11 gene; torf12 gene; torf13 gene; torf14 gene; torf15 gene; torf16 gene; torf17 gene; torf18 gene; torf19 gene; torf2 gene; torf20 gene; torf21 gene; torf22 gene; torf3 gene; torf4 gene; torf5 gene; torf6 gene; torf7 gene; torf8 gene; torf9 gene; tryptophan 2-monooxygenase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.
REFERENCE 1

AUTHORS Gielen J., Terryn N., Van Montagu M. and Villarroel R.
TITLE Complete nucleotide sequence of the T-DNA region of the plant tumor
inducing Agrobacterium tumefaciens Ti plasmid pTiC58
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 29524)
AUTHORS Gielen J.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-1999) Gielen J., Genetics, VIB/UG, KU
Leuven, Belgium
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RESULT 9
BD016312
LOCUS
DEFINITION Method of promoting plant transcription by using octopine T-DNA
ACCESSION BD016312.1 GI:22557450
VERSION JP 2001190289-A/1.
KEYWORDS Agrobacterium tumefaciens (Rhizobium radiobacter)
SOURCE Agrobacterium tumefaciens
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 24595)
AUTHORS Barker, R. F. and Kemp, J. D.
TITLE Method of promoting plant transcription by using octopine T-DNA
JOURNAL Patent: JP 2001190289-A 1 17-JUL-2001;
MYCOGEN PLANT SCIENCE INC
COMMENT OS Agrobacterium tumefaciens
PN JP 2001190289-A/1
PD 17-JUL-2001
PF 22-NOV-2000 JP 2000356816
PR 18-NOV-1983 US 553786
PI RICHARD F BARKER, JOHN D KEMP
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC Method of
promoting plant transcription by using octopine T-CC
DNA promoter
FH Key
FT source
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source location/Qualifiers
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Best Local Similarity 81.5%; Freq. No. 1.4e-295;
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RESULT 10
E00404
LOCUS E00404 24595 bp DNA linear PAT 29-SEP-1997
DEFINITION Ti plasmid T-DNA region.
ACCESSION E00404

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VERSION      E00404.1 GI:2168687
KEYWORDS     JP 1985156333-A/1..
SOURCE       Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM     Agrobacterium tumefaciens
              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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REFERENCE    1 (bases 1 to 24595)
AUTHORS      Garli, E.D., Deniau, D.S. and Richiyado, E.B.
TITLE        SELECTION USING OPINE SYNTHASE GENE
              Patent: JP 1985156333-A 1 16-AUG-1985;
              AGURIJENETIKUSU RES ASSOC LTD
JOURNAL      OS Agrobacterium tumefaciens
              PN JP 1985156333-A/1
COMMENT      PD 16-AUG-1985
              PF 14-SEP-1984 JP 1984193841
              PR 14-SEP-1983 US 83 532280
              PI GARII EB DAARU, DENISU DABURIYU SATSUTON,
              PI RICHIIYADO EFU BEIKAA
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              CC Topology: Linear;
              CC Key Location/Qualifiers
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DEFINITION	Sequence 1 from patent US 5428147.
ACCESSION	AR364803
VERSION	AR364803.1 GI:34427834
KEYWORDS	.
SOURCE	Unknown.

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 24595)
JOURNAL	Barker, R. F. and Kemp, J. D.
FEATURES	Ocrotropine T-DNA promoters.
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Query Match	49.9%	Score 958.4	DB 2	Length 24595
Best Local Similarity	81.5%	Pred. NO. 1.4e-299		
Matches 121; Conservative	0	Mismatches 261	Indels 16	Gaps 9

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ACCESSION	X00493	X05108	X00282
VERSION	X00493.1	GI:39062	
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SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
REFERENCE Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
AUTHORS 1 (bases 1 to 24595)
TITLE Barker, R.F., Idler, K.B., Thompson, D.V. and Kemp, J.D.
JOURNAL Nucleotide sequence of the T-DNA region from the Agrobacterium
AUTHORS 2 (bases 602 to 14237)
TITLE 2 (bases 602 to 14237)
JOURNAL Plant Mol. Biol. 2, 335-350 (1983)
AUTHORS Gijlen, J., De Beuckeleer, M., Seurinck, J., Deboeck, F., De Greve, H.,
Lemmers, M., Van Montagu, M. and Schell, J.
TITLE The complete nucleotide sequence of the T-DNA of the Agrobacterium
JOURNAL tumefaciens plasmid pTiAch5
AUTHORS EMBO J. 3 (4), 835-846 (1984)
PUBMED 6327292
TITLE 3 (bases 1 to 24595)
JOURNAL Turk, S.C., Nester, E.W. and Hooykaas, P.J.
AUTHORS The *virA* promoter is a host-range determinant in Agrobacterium
TITLE tumefaciens
JOURNAL Mol. Microbiol. 7 (5), 719-724 (1993)
PUBMED 8469115
TITLE 4 (bases 1 to 24595)
JOURNAL Guevara-Garcia, A., Mosqueda-Cano, G., Arguello-Ascorga, G.,
AUTHORS Simpson, J. and Herrera-Estrella, L.
TITLE Tissue-specific and wound-inducible pattern of expression of the
JOURNAL mannopine synthase promoter is determined by the interaction
AUTHORS between positive and negative cis-regulatory elements
JOURNAL Plant J. 4 (3), 495-505 (1993)
PUBMED 8220492
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Best Local Similarity 81.5%; Pred. No. 1.4e-299;
Matches 1221; Conservative 0; Mismatches 261; Indels 16; Gaps 9;
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ORGANISM	Agrobacterium tumefaciens		
ORGANISM	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.		
REFERENCE	1	(bases 193234 to 194140; 1 to 23692)	
REFERENCE	Barker, R.F., Idler, K.B., Thompson, D.V., and Kemp, J.D.		
REFERENCE	Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octopine Ti plasmid pTi15955		
REFERENCE	Plant Mol. Biol. 2, 335-350 (1983)		
REFERENCE	2	(bases 166443 to 168193)	
REFERENCE	original sequence presented in Genbank Accession Number X00493		
REFERENCE	Yanofsky, M.F. and Nester, E.W.		
REFERENCE	Molecular characterization of a host-range-determining locus from Agrobacterium tumefaciens		
REFERENCE	J. Bacteriol. 168 (1), 244-250 (1986)		
REFERENCE	3	(bases 168089 to 173951)	
REFERENCE	Yanofsky, M.F., Porter, S.G., Young, C., Albright, L.M., Gordon, M.P. and Nester, E.W.		
REFERENCE	The virD operon of Agrobacterium tumefaciens encodes a site-specific endonuclease		
REFERENCE	Cell 47 (3), 471-477 (1986)		
REFERENCE	4	(bases 175278 to 177719)	
REFERENCE	Winans, S.C., Allena, P., Stachel, S.E., McBride, K.E. and Nester, E.W.		
REFERENCE	Characterization of the virD operon of the Agrobacterium Ti plasmid pTiA6		
REFERENCE	Nucleic Acids Res. 15 (2), 825-837 (1987)		
REFERENCE	5	(bases 50125 to 54471)	
REFERENCE	Habeeb, L.F., Wang, L., and Winans, S.C.		
REFERENCE	Transcription of the octopine catabolism operon of the Agrobacterium tumor-inducing plasmid pTiA6 is activated by a LysR-type regulatory protein		
REFERENCE	Mol. Plant Microbe Interact. 4 (4), 379-385 (1991)		
REFERENCE	6	(bases 50125 to 54471)	
REFERENCE	Valdivia, R.H., Wang, L., and Winans, S.C.		
REFERENCE	Characterization of a putative periplasmic transport system for octopine accumulation encoded by Agrobacterium tumefaciens Ti plasmid pTiA6		
REFERENCE	173 (20), 6398-6405 (1991)		
REFERENCE	7	(bases 68024 to 76460)	
REFERENCE	Kim, K.S. and Farrand, S.K.		
REFERENCE	Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mannopine by Agrobacterium tumefaciens are homologs of the T-region genes responsible for synthesis of this opine by the plant tumor		
REFERENCE	J. Bacteriol. 178 (11), 3275-3284 (1996)		
REFERENCE	8	(bases 39167 to 45466)	
REFERENCE	Fuqua, C. and Winans, S.C.		
REFERENCE	Localization of OCCR-activated and Trar-activated promoters that express two ABC-type permeases and the trar gene of Ti plasmid		
REFERENCE	J. Microbiol. 20 (6), 1199-1210 (1996)		
REFERENCE	9	(bases 22855 to 39243; 96353 to 111409)	
REFERENCE	Alt-Morbe, J., Stryker, J.L., Fuqua, C., Li, P.L., Farrand, S.K. and Winans, S.C.		
REFERENCE	The conjugal transfer system of Agrobacterium tumefaciens octopine-type Ti plasmids is closely related to the transfer system of an IncP plasmid and distantly related to Ti plasmid vir genes		
REFERENCE	J. Bacteriol. 178 (14), 4248-4257 (1996)		
REFERENCE	10	(bases 54312 to 62806)	
REFERENCE	Oger, P., Kim, K.S., Sackett, R.L., Piper, K.R. and Farrand, S.K.		
REFERENCE	Octopine-type Ti plasmids code for a mannopine-inducible dominant-negative allele of trar, the quorum-sensing activator that regulates Ti plasmid conjugal transfer		
REFERENCE	Mol. Microbiol. 27 (2), 277-288 (1998)		
REFERENCE	11	(bases 133963 to 138972)	
REFERENCE	Kalogeraki, V.S. and Winans, S.C.		
REFERENCE	Wound-released chemical signals may elicit multiple responses from an Agrobacterium tumefaciens strain containing an octopine-type Ti plasmid		
REFERENCE	J. Bacteriol. 180 (21), 5660-5667 (1998)		
REFERENCE	12	(bases 76455 to 98723)	
REFERENCE	Ly, S.M., Jafri, S., and Winans, S.C.		
REFERENCE	Mannopine acid and agropinid acid catabolism region of the octopine-type Ti plasmid pTi15955		
REFERENCE	Mol. Microbiol. 31 (1), 339-347 (1999)		
REFERENCE	13	(bases 1 to 194140)	
REFERENCE	Winans, S.C., Zhu, J., Oger, P.M., Schrammeijer, B., Hooykaas, P.J. and Farrand, S.K.		
REFERENCE	Octopine-type Ti plasmid sequence		
REFERENCE	14	(bases 68024 to 76460)	
REFERENCE	Kim, K.-S.		
REFERENCE	Direct Submission		
REFERENCE	Submitted (10-JAN-1995) Kun-Soo Kim, Microbiology, University of Illinois at Urbana-Champaign, 1201 W. Gregory Dr., Urbana, IL 61801, USA		
REFERENCE	15	(bases 96353 to 111409)	
REFERENCE	Winans, S.C.		
REFERENCE	Direct Submission		
REFERENCE	Submitted (20-DEC-1995) Stephen C. Winans, Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA		
REFERENCE	16	(bases 39167 to 45466)	
REFERENCE	Fuqua, C.		
REFERENCE	Direct Submission		
REFERENCE	Submitted (07-FEB-1996) Clay Fuqua, Biology, Trinty University, 715 Stadium Dr., San Antonio, TX 78212, USA		
REFERENCE	17	(bases 54312 to 62806)	
REFERENCE	Kim, K.-S., Sackett, R.L. and Farrand, S.K.		
REFERENCE	Direct Submission		
REFERENCE	Submitted (04-JUN-1996) Crop Sciences, University of Illinois at Urbana-Champaign, 240 ERMU, 1201 W. Gregory Dr., Urbana, IL 61801, USA		
REFERENCE	18	(bases 186239 to 193239)	
REFERENCE	Zhu, J. and Winans, S.C.		
REFERENCE	Direct Submission		
REFERENCE	Submitted (17-NOV-1997) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA		

REFERENCE
AUTHORS 21 (bases 133963 to 138972; 176911 to 186244)
TITLE Szyker,J.U., Mantis,N.J., Kalojeraki,V.S. and Winans,S.C.
JOURNAL Direct Submission
Submitted (23-DEC-1997) Microbiology, Cornell University, Ithaca,
NY 14853, USA
REFERENCE
AUTHORS 22 (bases 22855 to 39243)
TITLE Winans,S.C.
JOURNAL Direct Submission
Submitted (03-AUG-1998) Microbiology, Cornell University, Wing
Hall, Ithaca, NY 14853, USA
REFERENCE
AUTHORS 23 (bases 62801 to 66985)
TITLE Oger,P.M.
JOURNAL Direct Submission
Submitted (29-DEC-1998) Crop Sciences, University of Illinois at
Urbana-Champaign, 361 ERMU, 1201, W. Gregory Dr., Urbana, IL 61801,
USA
REFERENCE
AUTHORS 24 (bases 110822 to 133968)
TITLE Zhu,J. and Winans,S.C.
JOURNAL Direct Submission
Submitted (18-AUG-1999) Section of Microbiology, Cornell
University, Wing Hall, Ithaca, NY 14853, USA
REFERENCE
AUTHORS 25 (bases 1 to 194140)
TITLE Zhu,J., Oger,P.M., Schrammelfer,B., Hooykaas,P.J., Farrand,S.K. and
Winans,S.C.
JOURNAL Direct Submission
Submitted (07-MAR-2000) Microbiology, Cornell University, Wing
Hall, Ithaca, NY 14853, USA
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9	720.4	37.5	5622	3	AAC86506
10	720	37.5	721	3	AAC86514
11	720	37.5	723	10	ACF58155
12	717	37.4	717	13	AD663261
13	583.8	30.4	723	13	ADT62691
14	583.6	30.4	720	13	AD662464
15	583.6	30.4	720	13	AD559368
16	583.6	30.4	720	13	AD662875
17	582.2	30.3	723	13	ADR42934
18	582.2	30.3	723	13	ADR42936

19	582.2	30.3	723	15	AEF15453	AEF15453	Isopenten
20	582.2	30.3	723	15	AEF15472	AEF15472	Isopenten
21	582	30.3	720	13	AD663295	AD663295	Bacterial
22	582	30.3	720	13	AD663280	AD663280	Bacterial
23	580.6	30.3	723	13	ADR42938	ADR42938	IPR-like
24	580.6	30.3	723	15	AEF15470	AEF15470	Isopenten
25	578.8	30.2	720	13	AD663275	AD663275	Bacterial
26	578.8	30.2	720	13	AD663279	AD663279	Bacterial
27	578.8	30.2	720	13	AD663294	AD663294	Bacterial
28	577.4	30.1	723	15	ADR42940	ADR42940	IPR-like
29	577.4	30.1	723	15	AEF15468	AEF15468	Isopenten
30	577.2	30.1	2595	11	ADJ98856	ADJ98856	IPR gene
31	577.2	30.1	2595	11	ADL73033	ADL73033	Agrobacte
32	577.2	30.1	2595	14	AD66862	AD66862	Isopenten
33	577.2	30.1	9323	10	ADJ98857	ADJ98857	Binary ve
34	577.2	30.1	9323	14	AD66863	AD66863	Plasmid p
35	554.4	28.9	777	13	AD663297	AD663297	Bacterial
36	551.2	28.7	745	2	AAV69757	AAV69757	Isopenten
37	549.8	28.7	3183	6	AAD33601	AAD33601	A. thalia
38	549.2	28.6	3182	6	AAD33336	AAD33336	A. thalia
39	546.6	28.5	3183	2	AA742919	AA742919	SAG12-1 p
40	546.6	28.5	3183	10	AD138701	AD138701	A. thalia
41	546.6	28.5	3183	14	ABD64248	ABD64248	Arabidops
42	545.4	28.4	723	3	AAD00619	AAD00619	Agrobacte
43	543.6	28.3	720	13	AD663266	AD663266	Bacterial
44	543.6	28.3	720	13	AD663290	AD663290	Bacterial
45	543.6	28.3	720	13	AD663262	AD663262	Bacterial

ALIGNMENTS

RESULT 1
ADT92127
ID ADT92127 standard; DNA; 1919 BP.
XX
XX ADT92127;
AC
XX
XX
DT 13-JAN-2005 (first entry)
XX
XX
DE A. tuneiensi isopentenyl transferase (ipt) encoding DNA.
XX
XX
KM Ipt; transgenic; plant; cytokinin; female reproduction;
KM isopentenyl transferase; plant breeding; gene; ds.
XX
XX
OS Agrobacterium tuneiensi.
XX
FH Key Location/Qualifiers
FT CDS 690..1409
FT /*tag= a
FT /*product= "ipt"
XX
PN WO2004090143-A2.
XX
PD 21-OCT-2004.
XX
XX 02-APR-2004; 2004WO-US010064.
PF
XX
PR 04-APR-2003; 2003US-0460718P.
XX
XX (PTON-) PIONEER HI-BRED INT INC.
PA
XX
XX Haben JE, Zinsmeister C, Tomes DT, Abblitt SE, Helentjaris TG;
PI Niu X;
PI
PI WPI; 2004-748771/73.
DR P-PSDB; ADT92128.
DR GENBANK; X14410.
XX
XX Producing transgenic plants capable of regulated expression of cytokinin-
PT modulating gene comprises transformation of plant cells with a genetic
PT construct capable of temporally- or spatially-regulated expression of
PT cytokinin modulating gene.

QY 1621 TCAAAATTAGCAAAAATTGTTAAAGGTTCTTTATGCGGTAGGTTGTCGACTTTTCAT 1680
DB 1621 TCAAAATTAGCAAAAATTGTTAAAGGTTCTTTATGCGGTAGGTTGTCGACTTTTCAT 1680
QY 1681 CATTTGCGGTAGGAGGATTCAGATTCATCACTAATGTTAAAAAGCCGAGAAATTTACGGG 1740
DB 1681 CATTTGCGGTAGGAGGATTCAGATTCATCACTAATGTTAAAAAGCCGAGAAATTTACGGG 1740
QY 1741 TGGTGCATTTAGTTTGGCCGTTCAACATGATTTTGGCAATGTTGGTAACCAAGCACTAGC 1800
DB 1741 TGGTGCATTTAGTTTGGCCGTTCAACATGATTTTGGCAATGTTGGTAACCAAGCACTAGC 1800
QY 1801 CAACCGTTGATATCACTTAATCGATGAGACCGTTCCCTTGGTGGGCTGCTC 1860
DB 1801 CAACCGTTGATATCACTTAATCGATGAGACCGTTCCCTTGGTGGGCTGCTC 1860
QY 1861 TTGATGATAGAGTGGCGTTCAGTTTATTAACGCCGGTTAGCATTAATAGACAACTT 1919
DB 1861 TTGATGATAGAGTGGCGTTCAGTTTATTAACGCCGGTTAGCATTAATAGACAACTT 1919

RESULT 2
AD055756
ID AD055756 standard; DNA; 1997 BP.
XX
AC AD055756;
XX
DT 15-JUN-2004 (first entry)
XX
DE Agrobacterium tumefaciens T-DNA [isopentenyl] transferase oncogene ipt.
XX
KW Transgenic plant; T-DNA oncogene; [isopentenyl] transferase; ipt;
KW expression cassette; tissue-preferred promoter;
KW developmental stage-preferred promoter; root growth; drought resistance;
KW seedling vigour; plant branching; gene; ds.
XX
OS Agrobacterium tumefaciens.
XX
FH Key Location/Qualifiers
FT CDS 688..1410
FT /tag= a
FT /product= "Isopentenyl transferase"
FT /EC_number= "3.5.1.27"
XX
PN WO2004000015-A2.
XX
PD 31-DEC-2003.
XX
PE 19-JUN-2003; 2003WO-US019301.
XX
PR 19-JUN-2002; 2002US-0389982P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Mankin SL, Da Costa E SilvaO;
XX
DR WPI: 2004-071655/07.
DR P-PSDB; AD055757.
XX
PT Improving plant performance, e.g. increased root growth, drought
PT resistance or seedling vigor comprising transforming a plant with an
PT isopentenyl transferase, a tryptophan monooxygenase or an indole
PT acetamide hydrolase.
XX
PS Claim 3; SEQ ID NO 1; 61bp; English.
XX
CC The invention relates to a method of improving plant characteristics by
CC transforming a plant with genes encoding an isopentenyl transferase (EC
CC 3.5.1.27), a tryptophan monooxygenase (EC 1.13.12.3) and/or an indole
CC acetamide hydrolase (EC 3.5.1). The method involves transforming a plant
CC cell with an expression cassette comprising an isopentenyl transferase
CC gene under the control of a tissue-preferred promoter or a developmental
CC stage-preferred promoter (but not a senescence-preferred promoter).

CC Alternatively, the plant cell is transformed with an expression cassette
CC comprising a tryptophan monooxygenase gene and/or an indole acetamide
CC hydrolase gene operably linked to a tissue-preferred promoter. After
CC transformation, the plant cells are regenerated to form a transgenic
CC plant comprising the expression cassette. The invention also relates to
CC expression cassettes for use in the method of the invention; the
CC transgenic plants generated, and seed produced by the transgenic plants.
CC The transgenes used in the method of the invention are preferably the
CC Agrobacterium tumefaciens T-DNA oncogenes ipt (isopentenyl transferase),
CC iaam (tryptophan monooxygenase) and iaah (indole acetamide hydrolase),
CC and the tissue-preferred promoters are preferably the Arabidopsis
CC thaliana GA4H promoter or a promoter derived from an Agrobacterium
CC rhizogenes rolB promoter. The methods of the invention are useful for
CC improving the characteristics of a transgenic plant; for example, they
CC can be used to increase a plant's root growth, increase its drought
CC resistance, increase seedling vigour, or increase or decrease a plant's
CC branching. The present sequence represents the Agrobacterium tumefaciens
CC T-DNA [isopentenyl] transferase (ipt) oncogene which is specifically
CC claimed for use in the methods and expression cassettes of the invention.
XX
XX Sequence 1997 BP; 567 A; 406 C; 441 G; 583 T; 0 U; 0 Other;
XX
Query Match 56.8%; Score 1089.8; DB 12; Length 1997;
Best Local Similarity 84.9%; Pred. No. 9.1e-269;
Matches 1270; Conservative 0; Mismatches 212; Indels 13; Gaps 4;
QY 2 GATCCCGTTACAAAGTATGACAGCTTTGTAAATTCATATTAATGCAATCTGATGTTTA 61
DB 1 GATCCGTATACAAAGTATGACAGCTTTGTAAATTCATATTAATGCAATCTGATGTTTA 60
QY 62 ATTAAGATGTAATGCGGTA---GAAATGATATTTATTTATTTATTTCTTCTACATAG 117
DB 61 ACMAAGAAAGTAATGCGGTAAAGAAAAATGATATGATATGATATGATATGATATGATG 120
QY 118 TTGAAGTTTGCATATATATGCTAATGTAATTAATAATTAATGTAATGCGGCAATTTGTT 177
DB 121 TTGAAGTTTGCATATATGAT-----GTATAGTAATAATATCAATGTCGATTTATTT 174
QY 178 CAATATGCGCGGTTATTTCAAAAATATCTTTGATTTTGTACGAGACAAACAGCTGCAG 237
DB 175 GAAATGCGACGTTATTTCAACATATCTTTGATTTGTAATGACAAATGACAAACAGCTGCAG 234
QY 238 AAGTAAATTAAGAACGCTGTTTAAAGAAATTTGATATATATGTCGCCAGCTATAGGGCC 297
DB 235 AAGTAAATTAAGAACGCTGTTTAAAGAAATTTGATATATATGTCGCCAGCTATAGGGAGC 294
QY 298 ATTAAAGTTCAATTTGAAATAGCGCCCTTATTTTGAAGTCTCATCAATCAATATATTA 357
DB 295 ATTAAAGTTCAATTTGAAATAGCGCCCTTATTTTGAAGTCTCATCAATCAATATATTA 353
QY 358 AAAAATATCTCACTCTGTGCGCAGCAATGATATTAACCGGAGAAAAAGTAGATAAT 417
DB 354 CAACAGATCTCACTCTGTGCGCAGCAATGATATTAACCGGAGAAAAAGTAGATAAT 413
QY 418 CGCGGAAAAAGCTGCCGAGATGGAATAGCGGCTTCCTGATTTGCTGATTTAGTCAGC 477
DB 414 CGCGGAAAAAGCTGCCGAGATGGAATAGCGGCTTCCTGATTTGCTGATTTAGTCAGC 473
QY 478 TTATATTTGACTTAAGGAGGCGCTGTTAGTGAACAAATGCTTCAAGGAGACAGCATG 537
DB 474 CTATATTTGACTTAAGGAGGCGCTGTTAGTGAACAAATGCTTCAAGGAGACAGCATG 533
QY 538 CCACACTTTTGTGAAAAACAAGTTGCTTTTGGGAGAACCTAAAGCCACTTGTCTTC 597
DB 534 CCACACTGTGTTGAAAAACAATGCTTTTGGGAGAACGTAAGCCAGTGTCTTC 593
QY 598 AAGAGAGAAATTCAGAGAGAGGAATATTAACGCTCTGTACAGACTTCTCTTGCGAA 657
DB 594 AATAAGGAAATTCAGAGAGAGGAATATTAACGCTCTGTGTATACACTTCTTAATCCAA 653
QY 658 AATCAATTTGATTTCAACATATGCG--AAGACGATGATATGATATTTTTCGATG 715
DB 654 AATCAATTTGATTTCAACATATGCG--AAGACGATGATATGATATTTTTCGATG 713

QY 716 AACTTGACAGGAAAGACATGACTCGATAGCTCTTCCAGCAGACATGCGCTTCCACT 775
Db 714 AACTTGACAGGAAAGACATGACTCGATAGCTCTTCCAGCAGACATGCGCTTCCACT 773
QY 776 CCTCGCTGATGCGGCTCCAAATGCTGCTCCAACTATTCACACGGAAGCGGCGAGCCAAC 835
Db 774 CTTTCGCTGATGCGGCTCCAAATGCTGCTCCAACTATTCACACGGAAGCGGCGAGCCAAC 833
QY 836 AGTGAAGAACTGAAAGAAAGCACTCGTCTGATCCTTGATGATGCGCTTGTGAAAAGG 895
Db 834 AGTGAAGAACTGAAAGAAAGCACTCGTCTGATCCTTGATGATGCGCTTGTGAAAAGG 893
QY 896 TATCATTAACGCCAAGCAAGCTCATGAAAGCGCTCATTCGCGAGGTGCACATCCAGAGC 955
Db 894 TATCATTAACGCCAAGCAAGCTCATGAAAGCGCTCATTCGCGAGGTGCACATCCAGAGC 953
QY 956 CAAGAGGCGGCTTATCTTGAGGAGGATCATGCTGCTGCTGAGTGCATGCGGCAAG 1015
Db 954 CCAGCGGCGGCTTATCTTGAGGAGGATCATGCTGCTGCTGAGTGCATGCGGCAAG 1013
QY 1016 TCGTTATTTGAAACGCGAATTTCTTGCGCATATTTTCGCAACGAGTTAGCAGACGAGA 1075
Db 1014 CAGTTATTTGAGTCCGAGATTTTCTTGCGCATATTTTCGCGAGTTAGCAGACGAGAGA 1073
QY 1076 GAGCTTATGAGCGTGGCCAAAGACCAAGTTAAGCAATGTTACGCCCTTGCAGAGTCT 1135
Db 1074 GACCTTATGAGCACTGGCCAAAGGCGCAAGTTAAGCAATGTTACGCCCTTGCAGAGTCT 1133
QY 1136 TTCTATTATCCAAAGTTGTTTCAACTTGGAGGAGGCTGCGCTGAGGCCCATATCTGA 1195
Db 1134 TTCTATTATCCAAAGTTGTTTCAACTTGGAGGAGGCTGCGCTGAGGCCCATATCTGA 1193
QY 1196 AGGAGTCGATGATATGATATGCTGCTGCTATTTGCTACCCAGAACGATACGCGCGA 1255
Db 1194 AGAGATGATGATATGATATGCTGCTGCTATTTGTTAGCAGAACGATACATCTCGA 1253
QY 1256 TATGCTATTTGAGCTCGACGACGATATGAGAAATTAATGTTTCAAGGTATCGCTCAGA 1315
Db 1254 TATGCTATTTGAGCTCGACGACGATATGAGAAATTAATGTTTCAAGGTATCGCTCAGA 1313
QY 1316 GTTCTATATCCATGCGGCTGCGACAGAAACAGAAATTCCTTGGTGGCGCGACAGCTGT 1375
Db 1314 GTATTCATTCATGACGCCGACAAAGAAATTCCTTGAATTAACGAGCGGCTTA 1373
QY 1376 CGAAGCGTTTGAAGAGACCAACCATTTGCAATGATGATGATGATGATGATGATGATG 1435
Db 1374 CGAGCGAATTCGAAGGTATTCATTCGGAATGATGATGATGATGATGATGATGATG 1433
QY 1436 TTGTCGCTATTTGAATGAAGATGCTGCTTGTGTTGTTGTTGTTGTTGTTGTTG 1490
Db 1434 CTGCTTCTATTTGAATGAAGATGCTGCAATGTTTGTAGCTTGTGTTGTTGTTG 1488

RESULT 3
ID AANS0182 standard; DNA; 24596 BP.
XX AANS0182;

XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 17-OCT-1991 (first entry)
XX Complete nucleotide sequence of the T-DNA region of the octopine Ti
DE plasmid pTi15955.
XX
KM Plant vector; transformation-inducing principle (TiP) gene;
XX octopine Ti plasmid, ss.
OS Agrobacterium tumefaciens; ATCC 15955.
XX
PN EPI45338-A.

XX 19-JUN-1985.
PD 16-NOV-1984; 84EP-00307969.
XX 18-NOV-1983; 83US-0053786.
PR (AGRK) AGRIGENTICS RES ASSOC LTD.
PA (LUBR) LUBRIZOL GENETICS INC.
PI Barker RF, Kemp JD;
XX WPI; 1985-148223/25.
DR
XX New DNA vectors contg. T-DNA sequence of octopine Ti plasmid - for
PT expression in plant cells to confer desirable properties to plants and
PT their cells.
XX
PS Claim 28; Fig 1; 87pp; English.
XX
CC The inventors claim a vector contg. a transformation-inducing principle
CC (TiP) gene from Ti plasmid pTi15955. The sequence of the T-DNA of the
CC octopine-type Ti plasmid has fourteen open reading frames bounded by
CC eukaryotic promoters, ribosome binding sites, and polyadenylation sites.
CC With the vectors, expression of structural foreign genes in plant cells
CC is promoted. The gene esp. encodes an insecticidal toxin identical to or
CC derived from the crystal protein of Bacillus thuringiensis. (Updated on
CC 25-MAR-2003 to correct PA field.) (updated on 24-OCT-2003 to standardise
CC OS field)
CC
SO Sequence 24596 BP; 6534 A; 5510 C; 5793 G; 6759 T; 0 U; 0 Other;
Query Match 49.9%; Score 958.4; DB 1; Length 24596;
Best Local Similarity 81.5%; Pred. No. 1.2e-234;
Matches 1221; Conservative 0; Mismatches 261; Indels 16; Gaps 9;
QY 1 GGATCCCGGTACAGATGATGACGCTTTGTGTAATTTGATATTAATGCAATCTGATGTT 60
Db 8082 GGATCCCGGTACAGATGATGACGCTTTGTGTAATTTGATATTAATGCAATCTGATGTT 8141
QY 61 AATACGATGTAATGCGGTAGAAATGTAATTTATGTAATTTATCTTACATGATGTTG 120
Db 8142 AATACGATGTAATGCGGTAGAAATGTAATTTATGTAATTTATCTTACATGATGTTG 8200
QY 121 AAGTTGCAATATATGCTATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
Db 8201 AAGTTGCAATATATGCTATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8259
QY 181 ATGCGCGCGTATTTGCA-----AATATGCTTATTTGTTAGAGAGACACGACTGCA 235
Db 8260 ATGCGCGCGTATTTGCA-----AATATGCTTATTTGTTAGAGAGACACGACTGCA 8319
QY 236 GGAAGTAATTAAGACGCTGTTGTAAGAAATTTGCTATCATATGTCGCCAGCTATAGG 295
Db 8320 GGAAGTAATTAAGACGCTGTTGTAAGAAATTTGCTATCATATGTCGCCAGCTATAGG 8379
QY 296 CCATTTAAGTCAATTTGTAATGACCGCCCTTATTTGACGCTTCATCAATGAATAT 355
Db 8380 ACAAATTAAGTCAATTTGTAATGACCGCCCTTATTTGACGCTTCATCAATGAATAT 8436
QY 356 TAAATAATATCTACTCTGTCGCGAGCAATGATTAATTAACCGAGAAAGTGAAGATA 415
Db 8437 TAAATAATATCTACTCTTTCGTATGTAATGATTAATTAATTAATTAATTAATTAAT 8495
QY 416 ATGCGGAAAAACGTCGCCGAGTGCATGATACGCGCTTCGATTTGCTGATTTAGTCA 475
Db 8496 AATGCGGAAAAACGTCGAGTGCATGATTAATTAATTAATTAATTAATTAATTAATTA 8555
QY 476 GCTTATTTGACTTAAGGAGTCCCTGTTAGTGCATAATGCTTTCAAGAGAGACGAT 535
Db 8556 GCTTATTTGACTTAAGGAGTCCCTGTTAGTGCATAATGCTTTCAAGAGAGACGAT 8615
QY 536 GCCCACACTTTGTTGAAAAACAAGTTGCTTTTGGGAAAGAACTTAAGCCACTTGCTCT 595


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QY 296 CCATTTAAGTTCATTTGTGAATAGCCGCTTATTTTGAAGCTGTCATCAATCAATAT 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 ACAATTAGTCA--TTGTAATAGTCTCCCTTAATTTTAAGACTGCATATCAAGAT 355
QY 356 TAAAAATATCTCACTGTGTGCGCAGCAATGATTAATTAACCGCAAAAAGTGAGTAA 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 356 TACAAAATATCTCACT--TTTGTGATGATATGATTAATCAAGATGAATGATACAGTAA 414
QY 416 ATGCGGAAAAAAGCGCCGAGTGCATGAATAGCGGCTCGATTTGCTGATTTAGTCA 475
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 AAGGTGAAAAAAGCTCATAGAGTGGCATGATTAATTTCTCTGATGATCCCAATTTATTTCA 474
QY 476 GCTTTATTTGACTTAAGGTGCCCTCGTACTGACAAATGCTTTCAAGAGACAGGCAT 535
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 GCTTTATTTGACTTAAGGTGCCCTCGTACTGACAAATGCTTTCAAGAGACAGGCAT 534
QY 536 GCCCCACACTTTGTTGAAAAACAAGTTGCCCTTTGGGAGAAAGCTTAAAGCACTGTGCT 595
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 GCCCCACACTTTGTTGAAAAACAAGTTGCCCTTTGGG-ATACGGTAAAGCAGTTGCACT 593
QY 596 TCAAGAGGAATATCGAGAAAGAAATTAACAGCTCTGCT-ACAGACTTCTCTGTGCG 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 594 TCAATTAATGAATTTCAAGG-AGACAATATAACCGCTCTGATTAACACAAATTTCTAATAT 652
QY 655 AAAAAATCAATTTGATTTCAATATCCG--AAGACCAATGATCTAGTCTAATTTTCCG 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 653 AAAAAATCAATTTGATTTCAATATCTGCAAAAACTTAAGAACCTGCAATTAATTTTCCG 712
QY 713 TCCAATTTGACAGAAAGAAACATGACAGTGCATAGCTTTGCCAGACAGACTGACCTCC 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 713 TCCAATTTGACAGAAAGAAAGACAGACCGCATAGCTTTGCCAGACAGACAGGCTTCC 772
QY 773 AGTCTCTCGCTGATGCGTCTCAATGCTGTCTCAACTATCAACCGAGACGGAGCAC 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 773 AGTCTCTCGCTGATGCGGTCCTCAATGCTGTCTCAACTATCAACCGAGACGGAGCAC 832
QY 833 AACAGTGAAGAATCTGAAGAAGAACGACTGCTGCTGACTTGAATATGCGCCCTTGTGTAA 892
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 833 AACAGTGAAGAATCTGAAGAAGAACGACTGCTGCTGACTTGAATATGCGCCCTTGTGTAA 892
QY 893 GGGATCATCTCAGCCCAAGAGCTCATGAACGCGCTCACTTGCAGAGTGACAAATCAAGA 952
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 893 GGGATCATCTCAGCCCAAGAGCTCATGAACGCGCTCACTTGCAGAGTGATTAATCAAGA 952
QY 953 GGCCAAAGCGGGCTTATTTCTTGAAGAGATCTATCTGTTGCTCAGGTGCATGGCCCA 1012
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 953 GGCCAAAGCGGGCTTATTTCTTGAAGAGATCTCACTCTGTTGCTCAACTGCATGGCCCG 1012
QY 1013 AAGTCGTTATTTGAACCGGGATTTTGTGCGATATTTATGGCAACGATTAAGACAGCA 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1013 AAGTCGTTATTTGAACCGGGATTTTGTGCGATATTTATGGCAACGATTAAGACAGCA 1072
QY 1013 AAAACGCTATTGGAGTGCAATTTTGTGCGATATTTATGGCCCAAGATTACCGGACCA 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1013 AAAACGCTATTGGAGTGCAATTTTGTGCGATATTTATGGCCCAAGATTACCGGACCA 1072
QY 1073 GGAGAGCTTTCATGAGCTGCGCAAGACAGAGTTAAGAGATGTTATCCGCTCTGCAGG 1132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1073 AGAAGCTTTCATGAGAGCGGCGCAAGGCGAGATTGAAGAGATGTTGCACCCGCTGCAGG 1132
QY 1133 TCTTTCTATTTATCCAAAGATTGTTCAACTTTGAGGAGCGCTCGGTGAGGCCCACT 1192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1133 CCATTCTATTTATCCAAAGATTGTTATCTTTGAATGAACCTCGGCTGAGGCCCACTCT 1192
QY 1193 GGAAGGATCGATGATATCGAATATGCGCTGCTATTTGCTACCGCAACCGATACAGCC 1252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1193 GGAAGGATCGATGATATCGAATATGCGCTGCTATTTGCTACCGCAACCGATACAGCC 1252
QY 1253 CGATATGCTATTTGAGCTGCAAGCAGATATGGAATTAATGATTCAGGTATGCTCA 1312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1253 AGATATGCTATTTGAGCTGCAAGCAGATATGGAATTAATGATTAATGGAATGCTCA 1312
QY 1313 GGAAGTTCTAATTCATGCGCGCTGACAGAGAACAGAAATTTCCCTTTGTTGGCGCGACAGC 1372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1313 GGAAGTTCTAATTCATGCGCGCTGACAGAGAACAGAAATTTCCCGCAAGTTTAAACGAGCGCG 1372
QY 1373 TGTGAAAGCGTTTGAAGACCACTTCGAAATGTGATGATGACCAAGTTTGTCTTCA 1432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 1373 TTTGACGAGATTCGAAGAGTCAATCCGTTGCGGAAGTATAGATTACCGACGCCGCGCG 1432
QY 1433 GACTTGCGCTAATTTGAATTAAGATGTTCTGTTTGTGTTGTTGTTGTTGTTGTTG 1490
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1433 CACCTGCTTCATCTGATTAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1490
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
AAN50226
ID AAN50226 standard; DNA; 24593 BP.
XX
AC AAN50226;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-OCT-1991 (first entry)
XX
XX Sequence of opine synthase gene.
XX
XX Plant vector; Ti plasmid; T-DNA; ss.
XX
XX Agrobacterium tumefaciens; Ti plasmid.
XX
XX EPl40556-A.
XX
XX 08-MAY-1985.
XX
XX 12-SEP-1984; 84EP-00306233.
XX
XX 14-SEP-1983; 83US-00532280.
XX
XX (AGRK ) AGRIGENETICS RES ASSOC LTD.
XX (LUBR ) LUBRIZOL GENETICS INC.
XX
XX Dahl GA, Sutton DW, Barker RF;
XX
XX WPI; 1985-112086/19.
XX
XX Plasmid contg. opine synthase gene for selection - and foreign DNA,
XX useful as vector for transforming plant cells.
XX
XX Disclosure; Page 212-217; 69pp; Japanese.
XX
XX Plant cells (and protoplasts) and plasmids contg. the DNA fragment which
XX includes an opine synthase gene plus a gene for antibiotic resistance are
XX claimed. These plasmids provide max. efficiency for transfer of foreign
XX genes and can be amplified in the plant genome. They do not contain genes
XX specifying tumour formation and will not spread antibiotic resistance
XX throughout the plant population. (Updated on 25-MAR-2003 to correct PF
XX field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-
XX 2003 to standardise OS field)
XX
XX Sequence 24593 BP; 6554 A; 5493 C; 5787 G; 6759 T; 0 U; 0 Other;

Query Match 49.7%; Score 953.6; DB 1; Length 24593;
Best Local Similarity 81.3%; Pred. No. 2e-233;
Matches 1218; Conservative 0; Mismatches 264; Indels 16; Gaps 9;

QY 1 GGATCCCGTTCACAGTATTCGACGTTTGTAAATTCATATTAATGCAATCTGATGTTT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8082 GGATCCGTTTACAGTATTCGACGTTTGTAAATTCATATTAATGCAATCTGATGTTT 8141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AATAACGAATGAATGCGGTAGAAATATGATTTTATTTATTTATCTTTCACTATGTTG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8142 AATAACGAATGAATGCGGTAGAAATATGATTTTATTTATTTATTTATTTATTTATTTG 8200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 AAGTTTGAATTAATGCTATGTAATAATTAATAATGATGACGCGCAATTTGTTCAA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8201 AAGTTTGAATTAATGCTATGTAATAATTAATAATGATGACGCGCAATTTGTTCAA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 8201 GAGTGGCGCAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ATGGCGCGGTATTTTCAA-----AAATATCTTTGATTTTGTAGAGAGCAACGACTGCA 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 8260 ATGGCAGCTGTATTTCACCATGAATTTTGTGATTTTTTACATTAACAATATATGCA 8319
 QY 236 GGAAGTAAATTAAGAAGCGCTGTTGTTAAGAAATGCTATCATATGTGCCAGTATAGG 295
 Db 8320 GGAAGTAAATTAAGAGCGCGTGTAAAAAATTCGAATCATATGTGCCAATATAGG 8379
 QY 296 CCATTTAAGTTCAATGTGAATAGCGGCCCTTATTTGACGCTCATCAATCAATAT 355
 Db 8380 ACAATTAAGTCA--TTGTAATAGTCTCCCTTATTTTAACGATCACTCAATCAAGTAT 8436
 QY 356 TAAAAAATATCTCACTCTGTCCGACAGCAATGATATATAACGCAAAAAAGTAGATA 415
 Db 8437 TACAAAATATCTCACT-TTTCGTCAATATGATGTAATCAGAACTGAATATGTAACAATA 8495
 QY 416 ATCGGGGAAAAAGCTGCCGAGTGCATATAGCGGCTCCGATATGCTGATTAAGTCA 475
 Db 8496 AACGTGAAAAAAGCTCATAGAGTGCATATATATCTCTGCATTCGCAATTTATTC 8555
 QY 476 GCTTATTTGACTTAAGGGTGGCCCTGTTAGTGAACAATTTGTTCAAGACAGCCAT 535
 Db 8556 GCTTATTTGACTTAAGTGTGCTTGTGATGACAAATGCTTTCAGAGACAGCCAT 8615
 QY 536 GCCCACACTTTGTTGAAAAACAAGTTGCTTTGGGAAGAACTTAAAGCCACTTGGCT 595
 Db 8616 GCCCACACTTTGTTGAAAAACAAGTTGCTTTGGG-ATACGGTAAAGCCAGTTGCACT 8674
 QY 596 TCAAGAGGAATATCGAGAGAGAAATATAAGCCTCTGGT-ACAGACTTCTCTTGTGC 654
 Db 8675 TCAATATGATTAATTCAGG-AGACAAATATACCGCTCTGATTAACCAATTTCTATAT 8733
 QY 655 AAAAATCAATTTGTATTCACAATATGCG--AAGACGATGATCTACGTTATTTTGG 712
 Db 8734 AAAAATCAATTTGTATTCACAATATGCGAAAAAATTAAGACCTGCACTTAATTTTGG 8793
 QY 713 TCCAATTTGACAGAGAAAGACATCGACTGAGTGTGTCGACAGACAGTGGCTGCC 772
 Db 8794 TCCAATTTGACAGAGAAAGACATCGACTGAGTGTGTCGACAGACAGTGGCTGCC 8853
 QY 773 AGTCTCTGCTCGATCGCGTCCAAATGCTGTCTCTCAACTATCAACCGAAGCGGGGAC 832
 Db 8854 AGTCTCTGCTCGATCGCGTCCAAATGCTGTCTCTCAACTATCAACCGAAGCGGAC 8913
 QY 833 AACAGTGAAGAAGCTGAAGAAGAAAGCACTGCTGTATACCTGTATGATGCCCTTTGGTAA 892
 Db 8914 AACAGTGAAGAAGCTGAAGAAGAAAGCACTGCTGTATGATGATGCCCTTTGGTGA 8973
 QY 893 GGGTATCATTAAGCAAGCAAGCTCATACGAGCTCATTTGGGAGGTGACAAATCAACA 952
 Db 8974 GGGTATCATTAAGCAAGCAAGCTCATTAAGCTCATTAAGCTCATTAAGCTCATTAAG 9033
 QY 953 GGCCAAAGCGGGCTTATTTCTGAGGAGAGATCTATCTCTGTGCTCAAGGTGATGGCGCA 1012
 Db 9034 GGCCAAAGCGGGCTTATTTCTGAGGAGAGATCTATCTCTGTGCTCAAGGTGATGGCG 9093
 QY 1013 AAGTGTATTTGAACCGCGGATTTTCGTTGGCATATATTCGCAACGAGTTGACAGACA 1072
 Db 9094 AAAAGCATTTGAGAGTGAAGATTTTCGTTGGAATTTATTCGCCCAAGTTACCCGACCA 9153
 QY 1073 GAGAGCTTCATGAGCGTGGCCCAAGACAGAGTTAAGACAGATTAAGCGCCCTCTGACAG 1132
 Db 9154 AGAGACCTTCATGAAGCGGCCCAAGGCCAGAGTTAAGAGAGTTGACACCCGCTGACAGG 9213
 QY 1133 TCTTTCTATTAACAAGATTGGTTCAACTTTGAGGAGGCTCGGCTGAGGCCCATCT 1192
 Db 9214 CCATTCTATTAATCAAGATTGGTTCATCTTTGATGATGAACCTCGGCTGAGGCCCATCT 9273
 QY 1193 GGAAGGATTCATGATATCATATATGCTGCTATTTGCTACCCGAACCATATACAGCC 1252
 Db 9274 GAAAGAGATCATGATATCATATATGCTGCTATTTGCTACCCGAACCATATACAGCC 9333
 QY 1253 CGATATGCTATTCAGCTCGACGAGATATGAGAAATTAATGATTCACGATATGCTCA 1312
 Db 9334 AGATATGCTATTCAGCTTCGACGAAATATGGAAGTGAAGTTGATTAATGGATGCTCA 9393

QY 1313 GGAAGTTTCAATTCATGCGCGTGCACAGACAGAAATTCCTTTGCTGGCGGCGACAGC 1372
 Db 9394 GGAAGTATTTCAATTCATGCGCGGCGCAACAGAAATTCCTTCAAGTTAAGCGACAGCCG 9453
 QY 1373 TGTGCAAGCGTTTGAAGACCAACATTCGAATGATGATGATGACCGAGTTTGTTCGA 1432
 Db 9454 TTTGCAAGCGATTCGAAGGTCATCCGTTGGAATGATGATGATGATGACCGAGCCCTGCTG 9513
 QY 1433 GACTTGTGCTATTTGAATTAAGATGTTGCTTTGTTGTTGTTGTTGTTGTTGTTG 1490
 Db 9514 CACCTGTCTATCTCGAATTAAGATGTTGCTATTTGTTGCTTTGCTTTGCTTTGCTG 9571
 RESULT 6
 AAC86511
 ID AAC86511 standard; DNA; 3017 BP.
 XX
 AC AAC86511;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
 XX
 KW temporal gene expression; spatial gene expression; plant seed;
 KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
 KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
 KW ipt; ss.
 XX
 OS Synthetic.
 OS Zea mays.
 OS Agrobacterium tumefaciens.
 XX
 PN WO20063401-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 13-APR-2000; 2000WO-US009943.
 XX
 PR 16-APR-1999; 99US-0129844P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Haben JE, Zinselmeier C, Tomes D;
 XX
 DR WPI; 2000-672743/65.
 XX
 PT Novel recombinant DNA construct useful for producing transgenic plants
 PT having enhanced levels of cytokinin expression, improved stress tolerance
 PT and yield stability.
 XX
 PS Disclosure; Page 72-73; 76pp; English.
 XX
 CC The present sequence represents a recombinant DNA molecule of the
 CC invention. It comprises, in this order, a maize promoter, an
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
 CC terminator. The DNA molecules of the invention comprise a genetic
 CC construct consisting of a promoter directing temporal and/or spatial gene
 CC expression in plant seed operatively linked to a cytokinin modulating
 CC gene. The recombinant DNA molecules are useful for producing fertile,
 CC transgenic plants capable of regulated expression of a cytokinin
 CC modulating gene in developing seeds. They are also useful for improving
 CC stress tolerance and yield stability in plants. The preferential
 CC expression of recombinant DNA molecules of the invention occurs about 14-
 CC 25 days after pollination. The transgenic plants thus produced have
 CC enhanced levels of cytokinin expression exhibit improved seed size,
 CC decreased tip kernel abortion and increased seed set during unfavourable
 CC environmental conditions
 CC
 SQ Sequence 3017 BP; 865 A; 679 C; 622 G; 851 T; 0 U; 0 Other;

Query Match 37.6%; Score 722; DB 3; Length 3017;
 Best Local Similarity 98.6%; Pred. No. 2.2e-174;

[illegible]

OS	Solanum tuberosum.
XX	
PN	WO20063401-A1.
PD	26-OCT-2000.
XX	
PE	13-APR-2000; 2000WO-US009943.
XX	
PR	16-APR-1999; 99US-0129844P.
XX	
PA	(PION-) PIONEER HI-BRED INT INC.
XX	
PI	Hadden JE, Zinselmeier C, Tomes D;
XX	
DR	WPI; 2000-672743/65.
XX	
PT	Novel recombinant DNA construct useful for producing transgenic plants
PT	having enhanced levels of cytokinin expression, improved stress tolerance
PT	and yield stability.
PS	Disclosure; Page 70-71; 76pp; English.
XX	
CC	The present sequence represents a recombinant DNA molecule of the
CC	invention. It comprises, in this order, a maize promoter, an
CC	Agrobacterium isopentenyl transferase (ipt) gene fragment, and a Solanum
CC	tuberosum terminator. The DNA molecules of the invention comprise a
CC	genetic construct consisting of a promoter directing temporal and/or
CC	spatial gene expression in plant seed operatively linked to a cytokinin
CC	modulating gene. The recombinant DNA molecules are useful for producing
CC	fertile, transgenic plants capable of regulated expression of a cytokinin
CC	modulating gene in developing seeds. They are also useful for improving
CC	stress tolerance and yield stability in plants. The preferential
CC	expression of recombinant DNA molecules of the invention occurs about 14-
CC	25 days after pollination. The transgenic plants thus produced have
CC	enhanced levels of cytokinin expression exhibit improved seed size,
CC	decreased tip kernel abortion and increased seed set during unfavourable
CC	environmental conditions
XX	
XX	
SQ	Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
Query Match	37.5%; Score 720.4; DB 3; Length 2722;
Best Local Similarity	99.9%; Pred. No. 5.5e-174;
Matches 721; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	688 CGATGAGTCTACGTCTAATTTTCGGTCCAATTGCACAGAAAGACATCGACTGCGATAG 747
DB	1523 CCATGAGTCTACGTCTAATTTTCGGTCCAATTGCACAGGAAGAATCGACTGCGATAG 1582
OY	748 CTCTTGCCAGCAGCATGCGCTCCCAAGTCTCTGCTGATCGGTCGAATGCTGTCTCTC 807
DB	1583 CTCCTGGCCAGCAGCATGCGCTCCCAAGTCTCTGCTGATCGGTCGAATGCTGTCTCTC 1642
OY	808 AACATATCAACCGGAAGCGGGGACCAACAGTGAAGAACTGAAGGAACGACCTGCTGTGT 867
DB	1643 AACATATCAACCGGAAGCGGGGACCAACAGTGAAGAACTGAAGGAACGACCTGCTGTGT 1702
OY	868 ACCCTGATGATCGGCCCTTTGGTAAAGGGTATCATTTACAGCCCAACAAGCTCATGAACGCGC 927
DB	1703 ACCTTGATGATCGGCCCTTTGGTAAAGGGTATCATTTACAGCCCAACAAGCTCATGAACGCGC 1762
OY	928 TCATTTGCGGAGGTGCACATCAACGAGGCCAAGCGGGCTTATTCTTGAGGAGGAGTCTTA 987
DB	1763 TCATTTGCGGAGGTGCACATCAACGAGGCCAAGCGGGCTTATTCTTGAGGAGGAGTCTTA 1822
OY	988 TCTGCGTTCCTCAGGTGCATGCGCGCAAGTCTTATTTGGAAGCGGATTTTCGTTGGCATTA 1047
DB	1823 TCTGCGTTCCTCAGGTGCATGCGCGCAAGTCTTATTTGGAAGCGGATTTTCGTTGGCATTA 1082
OY	1048 TTATTTGCGCAAGAGTTAGCACAGAGAGAGACTTCATGAGCGGTGGCCACAAGCAGAGTTTA 1107
DB	1883 TTATTTGCGCAAGAGTTAGCACAGAGAGAGACTTCATGAGCGGTGGCCACAAGCAGAGTTTA 1942
OY	1108 AGCAGATTTTACGCCCCCTCTGCGAGGTCTTCTTATATTCACAAGAGTGGTTCACATTGGA 1167

DB 1943 AGCAGATGTACGCCCTCTGCAGGCTTTCTATATCCAAAGTTGGTTCAACTTTGGA 2002
QY 1168 GGGAGCCTCGCTGAGAGCCCATCTAGAAAGGATCGATATGATGCTGCTAT 1227
DB 2003 GGGAGCCTCGCTGAGAGCCCATCTAGAAAGGATCGATATGATGCTGCTAT 2062
QY 1228 TTGCTAACCCAGAACGATCAAGCCCGATATGCTATTTGAGCTCCAGCGAATATGAGA 1287
DB 2063 TTGCTAACCCAGAACGATCAAGCCCGATATGCTATTTGAGCTCCAGCGAATATGAGA 2122
QY 1288 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGCTCAGAGAAACAGA 1347
DB 2123 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGCTCAGAGAAACAGA 2182
QY 1348 AATTCCTTTGGTGGGCGCGACAGCTGTGAAAGCGTTTGAAGAACCAACATTTCGATGT 1407
DB 2183 AATTCCTTTGGTGGGCGCGACAGCTGTGAAAGCGTTTGAAGAACCAACATTTCGATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244

RESULT 8
AAC86507
ID AAC86507 standard; DNA; 2722 BP.
AC AAC86507;
XX
DT 19-MAR-2001 (first entry)
XX
DE DNA comprising a barley promoter and Agrobacterium ipt gene.
XX
KW temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KW ipt; ss.
XX
OS Synthetic.
OS Hordeum vulgare.
OS Agrobacterium tumefaciens.
OS Zea mays.
XX
FN WO200063401-A1.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000MO-US009943.
XX
PR 16-APR-1999; 99US-0129844P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Haben JE, Zinselmeier C, Tomes D;
XX
DR WPI; 2000-672743/65.
XX
PT Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 69-70; 76pp; English.
XX
CC The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a barley promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
CC terminator. The DNA molecules of the invention comprise a genetic
CC construct consisting of a promoter directing temporal and/or spatial gene
CC expression in plant seed operatively linked to a cytokinin modulating
CC gene. The recombinant DNA molecules are useful for producing fertile,
CC transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving

CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions
XX
SQ Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
Query Match 37.5%; Score 720.4; DB 3; Length 2722;
Best Local Similarity 99.9%; Pred. No. 5.5e-174;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 668 CGATGATCTACGTTTAATTTTGGTCCAACTTGCAACAGAAAGACATGACTGCGATG 747
DB 1523 CCATGATCTACGTTTAATTTTGGTCCAACTTGCAACAGAAAGACATGACTGCGATG 1582
QY 748 CTCTGGCCGAGAGACTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGCTC 807
DB 1583 CTCTGGCCGAGAGACTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGCTC 1642
QY 808 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTCTGT 867
DB 1643 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTCTGT 1702
QY 868 ACCTGATGATGCGCCCTTTGGTAAAGGGTATCATTTACAGCCAAAGCTCATGAAAGCGC 927
DB 1703 ACCTGATGATGCGCCCTTTGGTAAAGGGTATCATTTACAGCCAAAGCTCATGAAAGCGC 1762
QY 928 TCATTGCGAGAGTGCAATCAATCAAGGCGCAAGGCGGCTTATTTAGGAGAGATCTA 987
DB 1763 TCATTGCGAGAGTGCAATCAATCAAGGCGGCTTATTTAGGAGAGATCTA 1822
QY 988 TCTCGTGTCTCAGAGTGCAATGCGCAAAAGTCTTATTTGGAACGCGATTTCGTTGCAATA 1047
DB 1823 TCTCGTGTCTCAGAGTGCAATGCGCAAAAGTCTTATTTGGAACGCGATTTCGTTGCAATA 1882
QY 1048 TTATTGCGAAGATTAGCAAGAGAGAGAGAGCTTCATGAGCGTGCCAAAGCAGAGTTA 1107
DB 1883 TTATTGCGAAGATTAGCAAGAGAGAGAGAGCTTCATGAGCGTGCCAAAGCAGAGTTA 1942
QY 1108 AGCAGATGTACGCCCCCTGACAGTCTTCTAATATCAAGATGTGTTCAACTTTGGA 1167
DB 1943 AGCAGATGTACGCCCCCTGACAGTCTTCTAATATCAAGATGTGTTCAACTTTGGA 2002
QY 1168 GGGAGCCTCGGCTGAGAGCCCATCTAGAAAGGATCGATATGATGCTGCTAT 1227
DB 2003 GGGAGCCTCGGCTGAGAGCCCATCTAGAAAGGATCGATATGATGCTGCTAT 2062
QY 1228 TTGCTAACCCAGAACGATCAAGCCCGATATGCTATTTGAGCTCCAGCGAATATGAGA 1287
DB 2063 TTGCTAACCCAGAACGATCAAGCCCGATATGCTATTTGAGCTCCAGCGAATATGAGA 2122
QY 1288 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGCTCAGAGAAACAGA 1347
DB 2123 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGCTCAGAGAAACAGA 2182
QY 1348 AATTCCTTTGGTGGGCGCGACAGCTGTGAAAGCGTTTGAAGAACCAACATTTCGATGT 1407
DB 2183 AATTCCTTTGGTGGGCGCGACAGCTGTGAAAGCGTTTGAAGAACCAACATTTCGATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244

RESULT 9
AAC86506
ID AAC86506 standard; DNA; 5622 BP.
AC AAC86506;
XX
DT 19-MAR-2001 (first entry)

XX DNA construct comprising a maize promoter and Agrobacterium ipt gene.
 DE temporal gene expression; spatial gene expression; plant seed;
 KM cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
 KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;
 KM ipt; ss.
 OS Synthetic.
 OS Zea mays.
 OS Agrobacterium tumefaciens.
 XX WO200063401-A1.
 PN 26-OCT-2000.
 PD 13-APR-2000; 2000WO-US009943.
 PF 16-APR-1999; 99US-0129844P.
 PR (PION-) PIONEER HI-BRED INT INC.
 PA Habben JE, Zinselmeier C, Tomes D;
 XX WPI; 2000-672743/65.
 DR Novel recombinant DNA construct useful for producing transgenic plants
 PT having enhanced levels of cytokinin expression, improved stress tolerance
 PT and yield stability.
 XX Disclosure; Page 67-69; 76pp; English.
 PS The present sequence represents a recombinant DNA molecule of the
 CC invention. It comprises, in this order, a maize promoter, an
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
 CC terminator. The DNA molecules of the invention comprise a genetic
 CC construct consisting of a promoter directing temporal and/or spatial gene
 CC expression in plant seed operatively linked to a cytokinin modulating
 CC gene. The recombinant DNA molecules are useful for producing fertile,
 CC transgenic plants capable of regulated expression of a cytokinin
 CC modulating gene in developing seeds. They are also useful for improving
 CC stress tolerance and yield stability in plants. The preferential
 CC expression of recombinant DNA molecules of the invention occurs about 14-
 CC 25 days after pollination. The transgenic plants thus produced have
 CC enhanced levels of cytokinin expression exhibit improved seed size,
 CC decreased tip kernel abortion and increased seed set during unfavourable
 CC environmental conditions
 CC
 XX Sequence 5622 BP; 1546 A; 1295 C; 1189 G; 1592 T; 0 U; 0 Other;
 SQ
 Query Match 37.5%; Score 720.4; DB 3; Length 5622;
 Best Local Similarity 99.9%; Pred. No. 7.3e-174;
 Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 988 TCTGTTGCTCAGGTGATGCGCCGAAGTGGTATTGGAAACGCGGATTTTCGTTGGATA 1047
 DB 1823 TCTGTTGCTCAGGTGATGCGCCGAAGTGGTATTGGAAACGCGGATTTTCGTTGGATA 1882
 QY 1048 TTATTCCCAACGATTAGCAGACGAGAGAGCTTCATAGCGTGCCCAAGACGAGTTA 1107
 DB 1883 TTATTCCCAACGATTAGCAGACGAGAGAGCTTCATAGCGTGCCCAAGACGAGTTA 1942
 QY 1108 AGCAGATGTTACGCCCTCTGACAGTCTTTCTATATTCACAAAGTTGGTTCACTTTGGA 1167
 DB 1943 AGCAGATGTTACGCCCTCTGACAGTCTTTCTATATTCACAAAGTTGGTTCACTTTGGA 2002
 QY 1168 GGGAGCCTCGGCTGAGGCCCATTAATGGAAGGATGATGATATGATATGATGATGAT 1227
 DB 2003 GGGAGCCTCGGCTGAGGCCCATTAATGGAAGGATGATGATATGATATGATGATGAT 2062
 QY 1228 TTGCTACCCCAACCAATCAGCGCCGATATGCTATTGACAGCTGACGAGATATGAGA 1287
 DB 2063 TTGCTACCCCAACCAATCAGCGCCGATATGCTATTGACAGCTGACGAGATATGAGA 2122
 QY 1288 ATAAATTGATTACGATATGCTATGCTCAGAGATTCTTAATCCATGCGCGTCGACAGACAGA 1347
 DB 2123 ATAAATTGATTACGATATGCTATGCTCAGAGATTCTTAATCCATGCGCGTCGACAGACAGA 2182
 QY 1348 AATTCCTTTGCTGCGGCGGACAGCTGTCCAAAGCGTTGAAAGGACCAACATTTGGAATGT 1407
 DB 2183 AATTCCTTTGCTGCGGCGGACAGCTGTCCAAAGCGTTGAAAGGACCAACATTTGGAATGT 2242
 QY 1408 GA 1409
 DB 2243 GA 2244
 RESULT 10
 ID AAC86514 standard; DNA; 721 BP.
 AC AAC86514;
 XX 19-MAR-2001 (first entry)
 DT
 XX Nucleotide sequence of an isopentenyl transferase (ipt) gene fragment.
 DE temporal gene expression; spatial gene expression; plant seed;
 KM cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
 KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;
 KM ipt; ss.
 XX
 XX Agrobacterium tumefaciens.
 OS
 XX WO200063401-A1.
 PN 26-OCT-2000.
 PD 13-APR-2000; 2000WO-US009943.
 PF 16-APR-1999; 99US-0129844P.
 PR (PION-) PIONEER HI-BRED INT INC.
 PA Habben JE, Zinselmeier C, Tomes D;
 XX WPI; 2000-672743/65.
 DR Novel recombinant DNA construct useful for producing transgenic plants
 PT having enhanced levels of cytokinin expression, improved stress tolerance
 PT and yield stability.
 XX Disclosure; Page 16; 76pp; English.
 PS The present sequence represents an isopentenyl transferase gene fragment.
 CC The fragment was used to produce the recombinant DNA molecules of the

CC invention. These comprise a genetic construct consisting of a promoter
CC directing temporal and/or spatial gene expression in plant seed
CC operatively linked to a cytokinin modulating gene. The recombinant DNA
CC molecules are useful for producing fertile, transgenic plants capable of
CC regulated expression of a cytokinin modulating gene in developing seeds.
CC They are also useful for improving stress tolerance and yield stability
CC in plants. The preferential expression of recombinant DNA molecules of
CC the invention occurs about 14-25 days after pollination. The transgenic
CC plants thus produced have enhanced levels of cytokinin expression exhibit
CC improved seed size, decreased tip kernel abortion and increased seed set
CC during unfavourable environmental conditions

XX Sequence 721 BP; 182 A; 176 C; 191 G; 172 T; 0 U; 0 Other;

Query Match 37.5%; Score 720; DB 3; Length 721;
Best Local Similarity 100.0%; Pred. No. 4.2e-174;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTTAATTTTGGTCCCACTTGCACAGGAAAGACATCGACTCGATAGCT 749
DB 2 ATGAGATCTACGCTTAATTTTGGTCCCACTTGCACAGGAAAGACATCGACTCGATAGCT 61
QY 750 CTTGCCACGACAGACTGAGCTCCCAAGTCTCTGCTCGATCGGCTCAATGCTCTCA 809
DB 62 CTTGCCACGACAGACTGAGCTCCCAAGTCTCTGCTCGATCGGCTCAATGCTCTCA 121
QY 810 CTATCAACCGGAAGCGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTCTGAC 869
DB 122 CTATCAACCGGAAGCGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTCTGAC 181
QY 870 CTTGATGATCGCCCTTTTGGTAAAGGGTATCATTTACAGCCACAGCATATGAAGGCTC 929
DB 182 CTTGATGATCGCCCTTTTGGTAAAGGGTATCATTTACAGCCACAGCATATGAAGGCTC 241
QY 930 ATTGGGAGGAGTGACAAATCAGAGGCGAAAGCGGGCTTATCTTGAGGAGAGATCTATC 989
DB 242 ATTGGGAGGAGTGACAAATCAGAGGCGAAAGCGGGCTTATCTTGAGGAGAGATCTATC 301
QY 990 TCGTGTCTCAGGTGATGAGCGCAAAAGTCGTTATTGGAACGCGGATTTTCTGTTGGCATATT 1049
DB 302 TCGTGTCTCAGGTGATGAGCGCAAAAGTCGTTATTGGAACGCGGATTTTCTGTTGGCATATT 361
QY 1050 ATTGCCAACGAGTTGACAGACAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGATTAAAG 1109
DB 362 ATTGCCAACGAGTTGACAGACAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGATTAAAG 421
QY 1110 CAGATGTTACGCGCCCTCTGACAGAGTCTTCTATTATCCAAAGATTGGTTCAACTTTGGAAG 1169
DB 422 CAGATGTTACGCGCCCTCTGACAGAGTCTTCTATTATCCAAAGATTGGTTCAACTTTGGAAG 481
QY 1170 GAGCCTCGGCTGAGGCGCCATACCTGGAAGGATCGATGATATCATATGCTCTGCTATTT 1229
DB 482 GAGCCTCGGCTGAGGCGCCATACCTGGAAGGATCGATGATATCATATGCTCTGCTATTT 541
QY 1230 GCTACCCAGAACCAAGATCAGCGCCCATATGCTATTGTCAGCTCGACGACAGATATGGAAT 1289
DB 542 GCTACCCAGAACCAAGATCAGCGCCCATATGCTATTGTCAGCTCGACGACAGATATGGAAT 601
QY 1290 AAATGATATTCACGAGTATGCTCTCAGAGTTTCTAATCCATGCGCGTGCACAGAAACAGAA 1349
DB 602 AAATGATATTCACGAGTATGCTCTCAGAGTTTCTAATCCATGCGCGTGCACAGAAACAGAA 661
QY 1350 TTCCCTTTGGTGGGCGCAGAGCTGTCGAAGGTTTGAAGACCAACATTTTGAATGTGA 1409
DB 662 TTCCCTTTGGTGGGCGCAGAGCTGTCGAAGGTTTGAAGACCAACATTTTGAATGTGA 721

RESULT 11
ACF58155
ID ACF58155 standard; cDNA; 723 BP.

XX ACF58155;
XX

DT 15-JAN-2004 (first entry)

XX Z. mays isopen1enyl transferase encoding cDNA.

XX Silk exser1en; plant; transformation; transgenic; gl2; cell division;

KW isopen1enyl transferase; gene; ss.

XX Zea mays.

XX Key Location/Qualifiers

FT CDS 1..723

FT /tag= a

FT /product= "isopen1enyl transferase"

XX WO2003087313-A2.

XX 23-OCT-2003.

XX 08-APR-2003; 2003WO-US010544.

XX 08-APR-2002; 2002US-0370796P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Zinselmeier C, Helencjaris TG;

XX WPI; 2003-845315/78.

XX P-PSDB; ABR61587.

PT Enhancing silk exser1en in a Zea mays plant under stress, relative to a

PT non-transformed Zea mays plant under stress by transforming the plant or

PT its ancestor with a construct comprising a silk-specific or silk-

PT preferred promoter.

XX Claim 2; Page 67-68; opp; English.

XX The invention relates to enhancing silk exser1en in a Zea mays plant

XX under stress, relative to a non-transformed Zea mays plant under stress.

XX The method involves transforming the plant or its ancestor with a

XX construct comprising a silk-specific or silk-preferred promoter operably

XX linked to a polynucleotide encoding a polypeptide that increases cell

XX division. The present sequence represents a cDNA encoding a Z. mays

XX isopen1enyl transferase, a polypeptide involved in cell division

XX Sequence 723 BP; 181 A; 176 C; 192 G; 174 T; 0 U; 0 Other;

Query Match 37.5%; Score 720; DB 10; Length 723;
Best Local Similarity 100.0%; Pred. No. 4.2e-174;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTTAATTTTGGTCCCACTTGCACAGGAAAGACATCGACTCGATAGCT 749
DB 1 ATGAGATCTACGCTTAATTTTGGTCCCACTTGCACAGGAAAGACATCGACTCGATAGCT 60
QY 750 CTTGCCACGACAGACTGAGCTCCCAAGTCTCTGCTCGATCGGCTCAATGCTCTCA 809
DB 61 CTTGCCACGACAGACTGAGCTCCCAAGTCTCTGCTCGATCGGCTCAATGCTCTCA 120
QY 810 CTATCAACCGGAAGCGGGCGACCAACATGGAAGAACTGAAGAAAGCACTGCTCTGAC 869
DB 121 CTATCAACCGGAAGCGGGCGACCAACATGGAAGAACTGAAGAAAGCACTGCTCTGAC 180
QY 870 CTTGATGATCGCCCTTTTGGTAAAGGGTATCATTTACAGCCAAAGCATCATGAAGCGCTC 929
DB 181 CTTGATGATCGCCCTTTTGGTAAAGGGTATCATTTACAGCCAAAGCATCATGAAGCGCTC 240
QY 930 ATTGGGAGGAGTGACAAATCAGAGGCGCAAGGCGGGCTTATCTTGAGGAGAGATATC 989
DB 241 ATTGGGAGGAGTGACAAATCAGAGGCGCAAGGCGGGCTTATCTTGAGGAGAGATATC 300
QY 990 TCGTGTCTCAGGTGATGAGCGCAAAAGTCGTTATTGGAACGCGGATTTTCTGTTGGCATATT 1049
DB 301 TCGTGTCTCAGGTGATGAGCGCAAAAGTCGTTATTGGAACGCGGATTTTCTGTTGGCATATT 360

QY 1050 ATTGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACGAGTTAAG 1109
CC ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACGAGTTAAG 1109
Db 361 ATTGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACGAGTTAAG 420
CC ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACGAGTTAAG 420
QY 1110 CAGATGTTAGCCCTCTGCGAGGCTTCTATTAATCCAGAGTTGGTTCACTTTGGAGG 1169
CC CAGATGTTAGCCCTCTGCGAGGCTTCTATTAATCCAGAGTTGGTTCACTTTGGAGG 1169
Db 421 CAGATGTTAGCCCTCTGCGAGGCTTCTATTAATCCAGAGTTGGTTCACTTTGGAGG 480
CC CAGATGTTAGCCCTCTGCGAGGCTTCTATTAATCCAGAGTTGGTTCACTTTGGAGG 480
QY 1170 GAGCTCGGCTGAGAGCCCATCTGGAAGGATCGATATGATATGCTGCTATTT 1229
CC GAGCTCGGCTGAGAGCCCATCTGGAAGGATCGATATGATATGCTGCTATTT 1229
Db 481 GAGCTCGGCTGAGAGCCCATCTGGAAGGATCGATATGATATGCTGCTATTT 540
CC GAGCTCGGCTGAGAGCCCATCTGGAAGGATCGATATGATATGCTGCTATTT 540
QY 1230 GCTACCCAGAACGAGATCAAGCCCGGATATGCTATTGCGAGCTCGAGCGAGATATGAGAA 1289
CC GCTACCCAGAACGAGATCAAGCCCGGATATGCTATTGCGAGCTCGAGCGAGATATGAGAA 1289
Db 541 GCTACCCAGAACGAGATCAAGCCCGGATATGCTATTGCGAGCTCGAGCGAGATATGAGAA 600
CC GCTACCCAGAACGAGATCAAGCCCGGATATGCTATTGCGAGCTCGAGCGAGATATGAGAA 600
QY 1290 AAATTGATTCACGGATATGCTCAGAGTTTCTAATCCATGCGCGTCGACAGAA 1349
CC AAATTGATTCACGGATATGCTCAGAGTTTCTAATCCATGCGCGTCGACAGAA 1349
Db 601 AAATTGATTCACGGATATGCTCAGAGTTTCTAATCCATGCGCGTCGACAGAA 660
CC AAATTGATTCACGGATATGCTCAGAGTTTCTAATCCATGCGCGTCGACAGAA 660
QY 1350 TTCCCTTTGGTGGGCGACAGAGCTGTGAGAGCGTTTGAAGACCACTTTGCAATGTA 1409
CC TTCCCTTTGGTGGGCGACAGAGCTGTGAGAGCGTTTGAAGACCACTTTGCAATGTA 1409
Db 661 TTCCCTTTGGTGGGCGACAGAGCTGTGAGAGCGTTTGAAGACCACTTTGCAATGTA 720
CC TTCCCTTTGGTGGGCGACAGAGCTGTGAGAGCGTTTGAAGACCACTTTGCAATGTA 720

RESULT 12
ADS63261
ID ADS63261 standard; cDNA; 717 BP.
AC ADS63261;
XX 02-DEC-2004 (first entry)
DT
XX
DE Bacterial polynucleotide #15248.
XX
KM Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 38935; 122bp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned
CC to provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
CC
XX
SQ Sequence 717 BP; 180 A; 176 C; 190 G; 171 T; 0 U; 0 Other;
Query Match 37.4%; Score 717; DB 13; Length 717;
Best Local Similarity 100.0%; Pred. No. 2.5e-173;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 690 ATGATCTACGCTTAATTTTGGTCAACTTGACAGAGAAAGACATGACTGCAATAGCT 749
Db 1 ATGATCTACGCTTAATTTTGGTCAACTTGACAGAGAAAGACATGACTGCAATAGCT 60
QY 750 CTTGCCAGACAGACTGCTCCAGTCTCTGCTCGATCGCGTCCAAATGCTGCTCA 809
Db 61 CTTGCCAGACAGACTGCTCCAGTCTCTGCTCGATCGCGTCCAAATGCTGCTCA 120
QY 810 CTATCAACCGGAGCGGCGGCAAGTGAAGAACTGAAGAGAGAGTCTGCTGAC 869
Db 121 CTATCAACCGGAGCGGCGGCAAGTGAAGAACTGAAGAGAGAGTCTGCTGAC 180
QY 870 CTTGATGATCCGCTTTGGTAAAGGATATCTTACAGCCAGCAAGCTCATGAACGAGCTC 929
Db 181 CTTGATGATCCGCTTTGGTAAAGGATATCTTACAGCCAGCAAGCTCATGAACGAGCTC 240
QY 930 ATTGGGAGGTGCAATCAGAGCCCAAGCGGCTTATCTTGAAGAGATATC 989
Db 241 ATTGGGAGGTGCAATCAGAGCCCAAGCGGCTTATCTTGAAGAGAGATATC 300
QY 990 TCGTTGCTCAGGTGATGCGGCAAAAGCTTATGGAACGGGATTTTGGTGGCATAT 1049
Db 301 TCGTTGCTCAGGTGATGCGGCAAAAGCTTATGGAACGGGATTTTGGTGGCATAT 360
QY 1050 ATTGCAACGAGTTAGCAGACGAGAGAGCTTGAAGCGTGGCCAGACGAGTTAAG 1109
Db 361 ATTGCAACGAGTTAGCAGACGAGAGAGCTTGAAGCGTGGCCAGACGAGTTAAG 420
QY 1110 CAGATGTTAGCCCTCTGCGAGGCTTCTATTAATCCAGAGTTGGTTCACTTTGGAGG 1169
Db 421 CAGATGTTAGCCCTCTGCGAGGCTTCTATTAATCCAGAGTTGGTTCACTTTGGAGG 480
QY 1170 GAGCTCGGCTGAGAGCCCATCTGGAAGGATCGATATGATATGCTGCTATTT 1229
Db 481 GAGCTCGGCTGAGAGCCCATCTGGAAGGATCGATATGATATGCTGCTATTT 540
QY 1230 GCTACCCAGAACGAGATCAAGCCCGGATATGCTATTGCGAGCTCGAGCGAGATATGAGAA 1289
Db 541 GCTACCCAGAACGAGATCAAGCCCGGATATGCTATTGCGAGCTCGAGCGAGATATGAGAA 600
QY 1290 AAATTGATTCACGGATATGCTCAGAGTTTCTAATCCATGCGCGTCGACAGAA 1349
Db 601 AAATTGATTCACGGATATGCTCAGAGTTTCTAATCCATGCGCGTCGACAGAA 660
QY 1350 TTCCCTTTGGTGGGCGACAGAGCTGTGAGAGCGTTTGAAGACCACTTTGCAATG 1406
CC TTCCCTTTGGTGGGCGACAGAGCTGTGAGAGCGTTTGAAGACCACTTTGCAATG 1406

Db 661 |||||
TTCCCTTGTGGCGCGCACAGCTGTCGAAGCGTTGAAGACCACTATTGGAATG 717

RESULT 13
ADT62691
ID ADT62691 standard; DNA; 723 BP.

AC ADT62691;

DT 13-JAN-2005 (first entry)

DE DNA encoding A. tumefaciens isopentenyl transferase (IPT).

KW DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
expression cassette; transgenic plant; transgenic;
isopentenyl transferase; IPT; ds.

OS Agrobacterium tumefaciens.

PN WO2004092390-A2.

PD 28-OCT-2004.

PF 09-APR-2004; 2004WO-US011000.

PR 09-APR-2003; 2003US-0461459P.

PA (MONS) MONSANTO TECHNOLOGY LLC.

PI Gilbertson L, Krieger E, Zhang W, Ye X;

DR WPI; 2004-758349/74.

PT New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
first border region linked to a transgene linked to an Agrobacterium Ti
plasmid second border region, useful for enhancing production of
transgenic plants.

PS Example 1; SEQ ID NO 2; 77pp; English.

XX The present invention relates to a DNA plasmid comprising a transfer DNA
CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
CC to at least one transgene linked to an Agrobacterium Ti plasmid second
CC border region, and located in the DNA plasmid outside of the T-DNA is a
CC plant expression cassette comprising a plant cell non-lethal negative
CC selectable marker gene linked to a vector backbone DNA. Also disclosed
CC are a method for enhancing the selection of transgenic plants that do not
CC contain vector backbone DNA, a method for reducing the copy number of a
CC transgene in a plant cell, and a transgenic plant produced by the method.
CC The DNA plasmid comprises the expression cassette comprising a promoter
CC that functions in plant cells operably linked to a plant cell non-lethal
CC negative selection marker gene. The promoter is a constitutive promoter.
CC The promoter expresses the linked non-lethal negative selection marker
CC gene product in tissue culture during plant regeneration. The plant cell
CC non-lethal negative selectable marker gene comprises a plant hormone
CC biosynthetic pathway gene, degradative gene, biosynthetic pathway
CC substrate-diverting gene or signalling gene, or metabolic interference
CC gene. The transgene is a plant positive selectable marker gene selected
CC from antibiotic resistance and herbicide resistance. The transgene
CC comprises a transgene of agronomic interest. The plant hormone
CC biosynthetic pathway gene is selected from gibberellic acid pathway
CC genes, cytokinin pathway genes, auxin pathway genes, ethylene pathway
CC genes, and abscisic acid pathway genes. The plasmid is useful for
CC enhancing the production of commercially viable transgenic plants. The
CC present sequence represents DNA encoding Agrobacterium tumefaciens
CC isopentenyl transferase (IPT) enzyme. This sequence is used as a non-
CC lethal negative selectable marker.

SQ Sequence 723 BP; 183 A; 166 C; 198 G; 176 T; 0 U; 0 Other;

Query Match 30.4%; Score 583.8; DB 13; Length 723;
Best Local Similarity 88.0%; Pred. No. 3.6e-139;

Matches 636; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTTAATTTTCGGTCCAACTTGACAGAAAGACATCGATCGATAGCT 749

Db 1 ATGATCTACGCTTAATTTTCGGTCCAACTTGACAGAAAGACATCGATCGATAGCT 60

QY 750 CTTGCCACAGACATCGGCTCCCACTCTCTGCTCGATCCGGTCCAAATGCTCTCTCA 809

Db 61 CTTGCCACAGACATCGGCTCCCACTCTCTGCTCGATCCGGTCCAAATGCTCTCTCA 120

QY 810 CTATCAACCGAAGCGGGGACCAACAGTGAAGAAGTGAAGAAGCACTGCTGTAC 869

Db 121 CTGTACACCGAAGCGGGGACCAACAGTGAAGAAGTGAAGAAGCACTGCTGTAC 180

QY 870 CTTGATGATCGCCCTTTGGTAAAGGTATCATTAACGCCAAGCTCATGACGCTC 929

Db 181 CTTGATGATCGCCCTTTGGTAAAGGTATCATTAACGCCAAGCTCATGACGCTC 240

QY 930 ATTGCGAGGTGCACATTCACAGGCCAAGCGGCTTATTCTTGAAGGAGATCTATC 989

Db 241 ATTGCGAGGTGCATATTAATTAATGAGGCCACAGCGGCTTATTCTTGAAGGAGATCTATC 300

QY 990 TCGTTGCTCAGGTGATGCGCGCAAGTGTATTGGAACGCGGATTTTGTGGCATATT 1049

Db 301 TCGTTGCTCAGGTGATGCGCGCAAGTGTATTGGAACGCGGATTTTGTGGCATATT 360

QY 1050 ATTGCAACGAGTTAGCAGACGAGAGCTTCATGAGCGTGGCCAGACAGAGTTAAG 1109

Db 361 ATTGCAACGAGTTAGCAGACGAGAGCTTCATGAGCGTGGCCAGACAGAGTTAAG 420

QY 1110 CAGATGTTACGCCCTCTGACAGGTCTTTCTATTAATCCAAAGTGTGTTCACTTGGAGG 1169

Db 421 CAGATGTTACGCCCTCTGACAGGTCTTTCTATTAATCCAAAGTGTGTTCACTTGGAGG 480

QY 1170 GAGCCTCGGCTGAGGCGCATCTGAGAGGATCGATGATATCATGATGCGCTGATTT 1229

Db 481 GAGCCTCGGCTGAGGCGCATCTGAGAGGATCGATGATATCATGATGCGCTGATTT 540

QY 1230 GCTACCCAGAACCAAGATCAAGCGCCGATATGCTATTGACAGCTGACAGATATGAGAA 1289

Db 541 GCTACCCAGAACCAAGATCAAGCGCCGATATGCTATTGACAGCTGACAGATATGAGAA 600

QY 1290 AATGATATTCACGGTATGCTTCAGAGATTTCTAATTCATGCGCGTGCAGAGAACGAAA 1349

Db 601 AAGTGAATTCATGAGATGCTTCAGAGATTTCTAATTCATGCGCGTGCAGAGAACGAAA 660

QY 1350 TTCCCTTGTGGCGCGCACAGCTGTCGAAGCGTTGAAGGACCAACATTGGAATGGA 1409

Db 661 TTCCCTTGTGGCGCGCACAGCTGTCGAAGCGTTGAAGGACCAACATTGGAATGGA 720

QY 1410 TAG 1412

Db 721 TAG 723

RESULT 14
ADS62464
ID ADS62464 standard; cDNA; 720 BP.

AC ADS62464;

DT 02-DEC-2004 (first entry)

DE Bacterial polynucleotide #14451.

KW Recombinant DNA construct; transformed plant; improved plant property;
cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
pathogen tolerance; pest tolerance; plant disease resistance;
cell cycle pathway modification; plant growth regulator;
homologous recombination; seed oil yield; protein yield; carbohydrate;
nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polynucleotide; gene; ss.

PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 35042; 122bp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 720 BP; 181 A; 166 C; 198 G; 175 T; 0 U; 0 Other;

Query Match 30.4%; Score 583.6; DB 13; Length 720;

Best Local Similarity 88.3%; Pred. No. 4e-139;

Matches 634; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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QY 690 ATGATACACGCTCTAATTTTGGTCCAACTTGCACAGGAAAGACATCCAGTCGATAGCT 749
DB 1 ATGATACGCGCTAATTTTGGTCCAACTTGCACAGGAAAGACATCCAGTCGATAGCT 60
QY 750 CTTGCCAGACACTGAGCTCCCACTGCTCTGCTGATCGGCTCAATGCTGCTCTCA 809
DB 61 CTTGCCAGACACTGAGCTCCCACTGCTCTGCTGATCGGCTCAATGCTGCTCTCA 120
QY 810 CTATCAACCGGAAGCGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 869
DB 121 CTGTCAACCGGAAGCGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTATAC 180
QY 870 CTTGATGATCGGCTTTGGTAAAGGATCATTAAGCCAAAGCCTCATGAAGGCTC 929
DB 181 CTTGATGATCGGCTTTGGTAAAGGATCATTAAGCCAAAGCCTCATGAAGGCTC 240
QY 930 ATTGGGAGGTGACAAATCAGAGGCAAGGCGGCTTATCTTGAGGAGGATCTATC 989
DB 241 ATTGGGAGGTGATATATATATAGGCCAGGCGGCTTATCTTGAGGAGGATCTATC 300
QY 990 TCGTGTCTCAGGTGATGAGCGGAAAGTCGTTATTTGAAACGCGGATTTTGGCATATT 1049
DB 301 TCGTGTCTCAGGTGATGAGCGGAAAGTCGTTATTTGAAAGTCGATTTTGGCATATT 360
QY 1050 ATTGCCAAGATTGACAGAGAGAGAGCTTCATGAGGTGCGCAAGCAGAGTTAAG 1109
DB 361 ATTGCCAAGATTGACAGAGAGAGAGCTTCATGAGGTGCGCAAGCAGAGTTAAG 420
QY 1110 CAGATGTTACGCGCTCTGACAGGTCTTTCTATTATCCAAAGATTGTTCACTTTGGAGG 1169
DB 421 CAGATGTTACGCGCTCTGACAGGTCTTTCTATTATCCAAAGATTGTTGAGAA 480
QY 1170 GAGCTCTGAGTGAAGGCCATCTGAAAGGATGATGATATGATATGATGCTGCTATT 1229
DB 481 GAGCTCTGAGTGAAGGCCATCTGAAAGGATGATGATATGATATGATGCTGTT 540
QY 1230 GCTACCCAGAACCAATACAGCGCGGATATGCTATTGACGTGACGAGATATGAGAAAT 1289
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DB 541 GCTACCCAGAACCAATACATCCGATATGCTATTGACGCTTGACGACAGATATGAGCAT 600
QY 1290 AAATTGATTACAGGTATGCTCAGAGATTCTAATTCATGCGCGTGCAGAGAAACAGAA 1349
DB 601 AAGTTGATTACAGGTATGCTCAGAGATTCTAATTCATGCGCGGACAGAAACAGAA 660
QY 1350 TTCCCTTTGTTGGGGGCGCACAGCTGTGAAAGCGTTTGAAGACCAACATTTGGAATGT 1407
DB 661 TTCCCTTGAGTTAACGACGCGCTTACGACGAGATTGAAAGGATTCATTCGGAATGT 718
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Search completed: June 26, 2006, 19:45:46
Job time : 1135 secs

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Db	8142	AAACAAGACGTAATGGCGTA-AAAAATGATATGTAATTAATTAATTAATTAATTAATG	8200
Qy	121	AAGTTGCAATTAATATGCTAATGTAAATTAATAAATATATGTAATGCGGATTTGTTCAA	180
Db	8201	GAGTGGCCGCAATATATGATGATTTATATTAATTAATAA--TATTTACTGTCACTATGACTGAG	8259
Qy	181	ATGGCCGCGTATTTTCAA-----AAATATCTTTGATTTTGTACGAGACACAGACTGCA	235
Db	8260	ATGGCACTGTTATTTTCAACCATGAAATTTTGTATTTTTCATAATTAACAAATTAATGCA	8319
Qy	236	GGAAGTAAATPAAAGACGCTGTGTTAAGAAATTGCTATCAATATATGTCGCCGATATAGG	295
Db	8320	GGAAGTAAATATATGAGCGCCGCTTTTAAATAATTCATCTATATGTGCTTACATATAGG	8379
Qy	296	CCATTTAAGTTCAATGTGAAATGACCGCCCTTATTTTGAAGTCTCATCAATCAATAT	355
Db	8380	ACATTTAAGTCAA---TTGTAAATAGTGTCTCCCTTATTTTAAGCACTCACTAATCAAGTAT	8436
Qy	356	TAAATAAATATCTCACTGTGTGCGCAGCATATGTAAATTAACCGAGAAAAGTGAAGTAA	415
Db	8437	TACAAATATCTCACT--TTTGTGATGATATGATTAATCAGAATGATATGTAACAAGTAA	8495
Qy	416	ATGCGGAAAAACGTCCGCGAGTGGCAATGAATACGGCCTCCGATATGCTGATTAATCA	475
Db	8496	AACGTGAAAAACGTCAATAGATGACATGAATTAATTCCTCTGCAATTCGCAATTAATCA	8555
Qy	476	GCTTATTTTGACTTAAGGGTGCCCTCGTATAGTGAACAATTGCTTTCAAGAGCAGCAT	535
Db	8556	GCTTATTTTGACTTAAGGTGCTCTCGTATGTCACAAATGCTTTCAAGAGAGCAGCAT	8615
Qy	536	GCCCCACACTTTGTTGAAAAACAGTTGCTTTTGGAGAGAACTTAAGCACAATTGCTCT	595
Db	8616	GCCCCACACTTTGTTGAAAAACAGTTGCTTTTGGG-ATACGGTAAAGCAGTTGACT	8674
Qy	596	TCAAGAGGAATATCGAGGAAGAAATTAACAACCTCTGGT-ACAGACTCTCTGTGCG	654
Db	8675	TCATTAATGAATTTTCAAGG-AGACAATTAACCCGCTCTGATTAACAATTTCTAATAT	8733
Qy	655	AAAAATCAATTTGATTTCAACATATACG--AAGACGATGGATCTAGCTTAATTTTCGG	712
Db	8734	AAAAATCAATTTGATTTCAATATATACGAAATAAATACTATGGAACCTGATCTAATTTTCGG	8793
Qy	713	TCCAACTTGCACAGAAAAGACATGACTGTCGATAGCTTCTTGCACGACAGACTGGCTCC	772
Db	8794	TCCAACCTGCACAGAAAAGACGACGACGCGATAGCTTCTTGCACGACAGCAGGCTTCC	8853
Qy	773	AGTCTCTCGCTCGATCGCGCTTCGAATGTGTCTTCAACTATCAACCGGAAGCGGCGAAC	832
Db	8854	AGTCTTTCGCTTATCGGATCGGATCGAATGTGTCTTCAACTATCAACCGGAAGCGGACAC	8913
Qy	833	AACAGTGAAACCTGAAGGAAGGAAGACTCGTCTGTGAACCTTATATGATGCGCCCTTTGTATAA	892
Db	8914	AACAGTGAAACCTGAAGGAAGGAAGAGCGCTCTTCACTTATATATGCGCTTCTGTGTGA	8973
Qy	893	GGGTATCATTTACAGCCCAAGCAAGCTCATGAACGGCTCATTTGCGAAGGTGCAATCA	952
Db	8974	GGGTATCATTTACAGCAAGCAAGCAAGCTCATTAAGCTGATCGAAGAGGTATATATCA	9033
Qy	953	GGCCAAAGCGCGGCTTATTTCTTGAAGGAGATCTATCTGTTGCTCAAGTGCATGGCGCA	1012
Db	9034	GGCCAAAGCGCGGCTTATTTCTTGAAGGAGATCTACCTCTGTGTCAACTGCATGGCGCG	9093
Qy	1013	AAGTCGTTATTTGAACGGCGGATTTTTCGTGGCATATTTATTCGCAACGATTAAGACGA	1072
Db	9094	AAACAGCTATTGAGTGACGATTTTTCGTGGCATATTTATTCGCAACAGTTAACCGACCA	9153
Qy	1073	GGAGAGCTTCAAGAGCGTGGCCCAAGACCAAGATTAAAGCAGATGTTAAGCCCTCTGACGG	1132
Db	9154	AGAGACCTTATGAAGAGCGGCCCAAGGCCAGAGTTTAAGCAGATGTTGACACCCCGTGCAGG	9213
Qy	1133	TCCTTTCTATTAACAAGATTGTTCAACTTTGAGGGAGCTCTGGCTGAGGCCCATACT	1192
Db	9214	CCATTTCTATTAATCAAGATTGTTTATCTTTGGAATGAACCTCGGCTGAGGCCCATTTCT	9273

Qy	1193	GAAAGGATCGATGATATTCCTATTCCTCCAGAAACGATCAGCC	1252
Db	9274	GAAAGAGATCGATGATATCGATATGCCATGTTGTTCTAGCCAGAACGATCAGCC	9333
Qy	1253	CGATATGCTATTGCAAGCTCGACGCGATATGAGATTAATGATTCACGGTATCGCTCA	1312
Db	9334	AGATATGCTATTGCAAGCTTGAACGCAAAATATGGAAGTAAATGATTAATGAGATCGCTCA	9393
Qy	1313	GGAGTTTCTAATCCATGCCGCGTCGACAGAAACAGAAATTCCTCTTGGTGGGCGGACAGC	1372
Db	9394	GGAGTATTTATCATCCATGCCGCGCCGCAACAGAAATATCCCCAAAGTTAAGCAGCGCC	9453
Qy	1373	TGTCGAAGCGTTGGAAGACCAACATTTGATGATGATATGACCAACATTTTGTTC	1432
Db	9454	TTTTCGACGATTCGAAGGTCATTCGGTTGGAAATGATTAATAGGTTACGCCACCGCTGCGTCG	9513
Qy	1433	GACTTGTGCGATTTTGAATAAAGATGTTGTTCTTGTGTGTGTGTGTGTGTATAG	1490
Db	9514	CACCTGTCTCATCTCGGATTAAGATGTTGCTAATGTTTGTGCTTGTGTGTGTGTGTG	9571

```

RESULT 2
US-09-545-334B-12
; Sequence 12, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; TITLE OF INVENTION: Seeds
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 3017
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, Genbank Accession #L22344;
; OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and
; OTHER INFORMATION: General Genetics 216:388-394 (1989); terminator from
; OTHER INFORMATION: Zea mays, Genbank Accession #L22345.
US-09-545-334B-12

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Query Match	37.6 %	Score 722	DB 4	Length 3017	
Best Local Similarity	98.6 %	Pred. No. 2e-205			
Matches 728	Conservative	0	Mismatch 10	Indels 0	Gaps 0
QY	672	CAACATATGCGACAGCCGATGGATCTACGCTCAATTTTTCGGTCCAACTTGACAGGAAAG	731		
Db	1390	CAACCCAGGATCCAAACATGGATCTACGCTCAATTTTTCGGTCCAACTTGACAGGAAAG	1449		
QY	732	ACATGACGTCGCAATACCTCTTGGCCAGAGATGGGCTCCAGTCTCTGCTGGATCGC	791		
Db	1450	ACATCGACTCGCATACCTCTTGGCCAGAGATGGGCTCCAGTCTCTGCTGGATCGC	1509		
QY	792	GTCCAATGCTGTCCTCAACTATCAACCGGAGCGGGCGACCAACGTGGAAGAACTGAA	851		
Db	1510	GTCCAATGCTGTCCTCAACTATCAACCGGAGCGGGCGACCAACGTGGAAGAACTGAA	1569		
QY	852	GGAGACGCTGCTGTAACCTTGATGATGCGCCCTTTGGTAAAGGGATCATTTACAGCCAA	911		
Db	1570	GGAGACGCTGCTGTAACCTTGATGATGCGCCCTTTGGTAAAGGGATCATTTACAGCCAA	1629		
QY	912	CAAGCTCATGACAGGCTCAATTGGCGAGGTGCACATCAACGAGGCCAAGGCGGGCTTATT	971		
Db	1630	CAAGCTCATGACAGGCTCAATTGGCGAGGTGCACATCAACGAGGCCAAGGCGGGCTTATT	1689		

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QY 972 CTTGAGGAGATCTATCTCGTGTCTCAGGTGATGCGCAAGTCGTTATTGGAACGCG 1031
DB 1690 CTTGAGGAGATCTATCTCGTGTCTCAGGTGATGCGCAAGTCGTTATTGGAACGCG 1749
QY 1032 GATTTTCGTTGGCATATTTATTGCAACGAGTTAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
DB 1750 GATTTTCGTTGGCATATTTATTGCAACGAGTTAGAGAGAGAGAGAGAGAGAGAGAGAG 1809
QY 1092 GCCAAGACCAAGATTAAAGAGAGATTACGCCCCCTGCAAGTCTTTCTATTATCCAAAG 1151
DB 1810 GCCAAGACCAAGATTAAAGAGAGATTACGCCCCCTGCAAGTCTTTCTATTATCCAAAG 1869
QY 1152 TTGTTTCAACTTTTGAGAGGAGCTTCGCTGAGGCCCCATATCTGAAAGGATTCAGATGAT 1211
DB 1870 TTGTTTCAACTTTTGAGAGGAGCTTCGCTGAGGCCCCATATCTGAAAGGATTCAGATGAT 1929
QY 1212 CGATATGCCCTGCTATTTTGCTACCGAGAACGATCAGCCCGGATATGCTATTGAGAGCTC 1271
DB 1930 CGATATGCCCTGCTATTTTGCTACCGAGAACGATCAGCCCGGATATGCTATTGAGAGCTC 1989
QY 1272 GACGAGATATGAGAAATTAATTGATTCACGCTATCGCTCAGAGATTCTAATCCATGCG 1331
DB 1990 GACGAGATATGAGAAATTAATTGATTCACGCTATCGCTCAGAGATTCTAATCCATGCG 2049
QY 1332 CGTGACACAGAAACAGAAATTCCTTTGCTGGCGCGACAGCTGTGCAAGCGTTTGAAGA 1391
DB 2050 CGTGACACAGAAACAGAAATTCCTTTGCTGGCGCGACAGCTGTGCAAGCGTTTGAAGA 2109
QY 1392 CCACCATTTTCCGATGTGA 1409
DB 2110 CCACCATTTTCCGATGTGA 2127

RESULT 3
US-09-545-334B-8
; Sequence 8, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselemer, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Hordeum vulgare, Plant Journal 6:849-860
; OTHER INFORMATION: (1994); gene from Agrobacterium tumefaciens, Molecular
; OTHER INFORMATION: and General Genetics 216:388-394 (1989); terminator
; OTHER INFORMATION: from Zea mays, Genbank Accession #S78780.
US-09-545-334B-8
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Query Match 37.5%; Score 720.4; DB 4; Length 2722;
Best Local Similarity 99.9%; Pred. No. 5.8e-205;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 668 CGATGATCTACGCTTAATTTTGGTCCAACTTGACACAGAAAGACATGACTGCGATG 747
DB 1523 CCATGATCTACGCTTAATTTTGGTCCAACTTGACACAGAAAGACATGACTGCGATG 1582
QY 748 CTCTTGCCAGCAGCTGCGCCCGAGTCTCTGCTGATGCGCTCAATGCTGCTC 807
DB 1583 CTCTTGCCAGCAGCTGCGCCCGAGTCTCTGCTGATGCGCTCAATGCTGCTC 1642
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QY 808 AACTATCAACCGGAAGCGGCGACCAACAGTGGAAAGAACTGAAGAAACGACTGCTGT 867
DB 1643 AACTATCAACCGGAAGCGGCGACCAACAGTGGAAAGAACTGAAGAAACGACTGCTGT 1702
QY 868 ACCTTGATGATCGCCCTTTGGTAAAGGGTATCATTTACGCCAAGCACTCATGAAGCGC 927
DB 1703 ACCTTGATGATCGCCCTTTGGTAAAGGGTATCATTTACGCCAAGCACTCATGAAGCGC 1762
QY 928 TCATTGCGAGAGTGCACAATCAACGAGCGCAAGGCGGCTTATTTCTTGAGGAGAGATCTA 987
DB 1763 TCATTGCGAGAGTGCACAATCAACGAGCGCAAGGCGGCTTATTTCTTGAGGAGAGATCTA 1822
QY 988 TCTGCTGCTCAGGTGATGCGCGCAAGTCTTATTGGAACGCGGATTTTCTGTTGCATA 1047
DB 1823 TCTGCTGCTCAGGTGATGCGCGCAAGTCTTATTGGAACGCGGATTTTCTGTTGCATA 1882
QY 1048 TTATTGCAAGAGATTAGCAGACGAGAGACTTCATGAGGCTGCCAAGCCAGAGTTA 1107
DB 1883 TTATTGCAAGAGATTAGCAGACGAGAGACTTCATGAGGCTGCCAAGCCAGAGTTA 1942
QY 1108 AGCAGATGTACGCCCTCTGCAAGTCTTTCTAATTATCAAGAGTTGTTCAACTTTGA 1167
DB 1943 AGCAGATGTACGCCCTCTGCAAGTCTTTCTAATTATCAAGAGTTGTTCAACTTTGA 2002
QY 1168 GGGAGCTCGGCTGAGGCCCATTACTGGAAGGATGATGATATGATATGCTGCTAT 1227
DB 2003 GGGAGCTCGGCTGAGGCCCATTACTGGAAGGATGATGATATGATATGCTGCTAT 2062
QY 1228 TTGCTACCCAGAACCAATCAACGCCCATATGCTATTGCTGACTGAGCGCAATATGAGA 1287
DB 2063 TTGCTACCCAGAACCAATCAACGCCCATATGCTATTGCTGACTGAGCGCAATATGAGA 2122
QY 1288 ATAAATGATTCACGCTATCGCTCAGAGATTCTAATCATGCGGCTGACAGAAACAGA 1347
DB 2123 ATAAATGATTCACGCTATCGCTCAGAGATTCTAATCATGCGGCTGACAGAAACAGA 2182
QY 1348 AATTCCTTTTGTGGCGCGACAGCTGTGCAAGCGTTTGAAGACACCACTTTGCAATGT 1407
DB 2183 AATTCCTTTTGTGGCGCGACAGCTGTGCAAGCGTTTGAAGACACCACTTTGCAATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244
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RESULT 4
US-09-545-334B-9
; Sequence 9, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselemer, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648;
; OTHER INFORMATION: gene from Agrobacterium tumefaciens, Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989); terminator from Solanum
; OTHER INFORMATION: tuberosum, Plant Cell 1(1):115-122 (1989).
US-09-545-334B-9
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Query Match	37.5%	Score 720.4	DB 4	Length 2722	
Best Local Similarity	99.9%	Pred. No. 5.8e-205			
Matches 721	Conservative 0	Mismatches 1	Indels 0	Gaps 0	
QY	688	CGATGATCTAAGCTTAATTTTCGGTCCAACTTGCACAGGAAAGACATCGACTCGATAG	747		
Db	1523	CCATGGATCTACGCTTAATTTTCGGTCCAACTTGCACAGGAAAGACATCGACTCGATAG	1582		
QY	748	CTCTTGGCCAGACACGTGGCCCTCCAGTCCCTCGTGCAGACGGGTCCAAAGCTGCTCTC	807		
Db	1583	CTCTTGGCCAGACACGTGGCCCTCCAGTCCCTCGTGCAGACGGGTCCAAAGCTGCTCTC	1642		
QY	808	AACATATCAACCGGAAGCGGGCGACCAACAGTGGAAAGAACTGAAAGCAACGCTGCTGT	867		
Db	1643	AACATATCAACCGGAAGCGGGCGACCAACAGTGGAAAGAACTGAAAGCAACGCTGCTGT	1702		
QY	868	ACCTTGATGATGCGCTTTGGTAAAGGGTATCATTTACAGCCAGCAAGCTCATGAACGGC	927		
Db	1703	ACCTTGATGATGCGCTTTGGTAAAGGGTATCATTTACAGCCAGCAAGCTCATGAACGGC	1762		
QY	928	TCATTGGGAGAGTGCACATACGAGGCGCAAGGCGGGCTTAATCTTGAGGAGAGATCTA	987		
Db	1763	TCATTGGGAGAGTGCACATACGAGGCGCAAGGCGGGCTTAATCTTGAGGAGAGATCTA	1822		
QY	988	TCTGTGTTGCTCAGGTGCATGCGCAAGTCGTTATTGGAAACGCGGATTTTCGTTGCATTA	1047		
Db	1823	TCTGTGTTGCTCAGGTGCATGCGCAAGTCGTTATTGGAAACGCGGATTTTCGTTGCATTA	1882		
QY	1048	TTATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCTTGCCCAACGACAGTTTA	1107		
Db	1883	TTATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCTTGCCCAACGACAGTTTA	1942		
QY	1108	AGCAGATGTTACGGCCCTCTGACAGTCTTCTATATATCAGAGTGGTTCAACTTTGGA	1167		
Db	1943	AGCAGATGTTACGGCCCTCTGACAGTCTTCTATATATCAGAGTGGTTCAACTTTGGA	2002		
QY	1168	GGGAGCCTCGGCTGAGGCGCCATCTAGTGAAGGATCGATGATATCGATATCCCTGCTAT	1227		
Db	2003	GGGAGCCTCGGCTGAGGCGCCATCTGAGAAAGGATCGATGATATCGATATCCCTGCTAT	2062		
QY	1228	TTGCTATCCAGAACCAATATCAGCCGCCATATATGCTATTTCAGCTGACGACCAATATGAGA	1287		
Db	2063	TTGCTATCCAGAACCAATATCAGCCGCCATATATGCTATTTCAGCTGACGACCAATATGAGA	2122		
QY	1288	ATTAATGATTCACGAGTATCGCTCAGAGTTTCTAATCCATGACGGCGTGCAGAGAACAGA	1347		
Db	2123	ATTAATGATTCACGAGTATCGCTCAGAGTTTCTAATCCATGACGGCGTGCAGAGAACAGA	2182		
QY	1348	AATTCCTCTTGGTGGCGCGACAGCTGTTCGAAGCGTTTGAAGACCAACATTTGCAGATGT	1407		
Db	2183	AATTCCTCTTGGTGGCGCGACAGCTGTTCGAAGCGTTTGAAGACCAACATTTGCAGATGT	2242		
QY	1408	GA 1409			
Db	2243	GA 2244			
RESULT 5					
US-09-545-334B-7					
Sequence 7, Application US/09545334B					
Patent No. 6992237					
GENERAL INFORMATION:					
APPLICANT: Zinselmeyer, Chris					
APPLICANT: Haben, Jeff					
APPLICANT: Tomes, Dwight					
TITLE OF INVENTION: Regulated Expression of Genes in Plant					
FILE REFERENCE: 0803					
CURRENT APPLICATION NUMBER: US/09/545.334B					
CURRENT FILING DATE: 2000-04-07					
PRIOR APPLICATION NUMBER: US 60/129,844					
PRIOR FILING DATE: 1999-04-16					

[illegible]

Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: Transgenic Seedless Plants
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,587
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,725
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..725
US-09-073-587-4

Query Match 28.7%; Score 551.2; DB 3; Length 745;
Best Local Similarity 84.1%; Pred. No. 1.5e-154;
Matches 622; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 688 CGATGATCTACGTTAATTTTGGTCCCACTTGACACAGAAAGACATCGACTGCGATAG 747
DB 1 CCATGAGACCTGCATTAATTTTGGTCCCACTTGACACAGAAAGACGACCGGATAG 60
QY 748 CTCTGGCCAGAGAGTGGCCCTCCAGTCCCTCGCTGATGCGCTCCAAAGCTTCTC 807
DB 61 CTCTGGCCAGAGAGTGGCCCTCCAGTCCCTCGCTGATGCGCTCCAAAGCTTCTC 120
QY 808 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTGT 867
DB 121 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAAAGACGCTCT 180
QY 868 ACCTTGATGATGCGCTTGTGTAAGGATCATTAACAGCCAGCAAGCTCATGAAGGC 927
DB 181 ACCTTGATGATGCGCTTGTGTAAGGATCATTAACAGCCAGCAAGCTCATGAAGGC 240
QY 928 TCATGCGGAGGTGACAAATACGAGGCCAAAGGGGCTTATTTTGAAGGAGATCTA 987
DB 241 TGATGAGAGGTGATTAATCATGAGGCCCAACGCGGGCTTATTTTGAAGGAGATCTA 300
QY 988 TCTCGTCTCAGTGCATGCGCAAGTGTATTGGAACGCGGATTTTCGTTGGCATA 1047
DB 301 CCTGCTCTCAACTGATGCGGCGAAGAGCTATTGGAAGTGCATTTTCGTTGGCATA 360

QY 1048 TTATTCGACAGATTTAGCAGACGAGAGACTTCATAGCGCTGGCCAAAGCCAGATTA 1107
DB 361 TTATTCGACAGATTTAGCAGACGAGAGACTTCATAGCGCTGGCCAAAGCCAGATTA 420
QY 1108 AGCAGATGTTAGCGCCCTCTCAGAGTCTTTCTATTTATCAAGAGTTGGTCACTTGA 1167
DB 421 AGCAGATGTTAGCGCCCTCTCAGAGTCTTTCTATTTATCAAGAGTTGGTCACTTGA 480
QY 1168 GGGAGCTCGGCTGAGGCCCATTAAGGAGATGATGATATGATATGCTGCTAT 1227
DB 481 ATGAACCTCGGCTGAGGCCCATTAAGGAGATGATGATATGATATGCTGCTAT 540
QY 1228 TTGCTACCCAGAACCAATTCAGGCCCATTAAGGAGATGATGATATGCTGCTAT 1287
DB 541 TTGCTACCCAGAACCAATTCAGGCCCATTAAGGAGATGATGATATGCTGCTAT 600
QY 1288 ATAAATGATTCACAGTATGCTGCTGAGAGTTCTTAATCATGCGGCTGACAGAAACAGA 1347
DB 601 GTAGTTATTAATGAGATTCGCTCAGAGTATTTTCATCATTCGCGCCAAACAGAAACAGA 660
QY 1348 AATTCCTTTGTGGGCGGACAGCTGTGGAAGCGTTTGAAGAACCAACATTTGAAATGT 1407
DB 661 AATTCCTTTGTGGGCGGACAGCTGTGGAAGCGTTTGAAGAACCAACATTTGAAATGT 720
QY 1408 GATGATTCACACCACTTTG 1427
DB 721 ATTAGTTACGCCAGCCCTG 740

RESULT 7
US-08-971-395-1
Sequence 1, Application US/08971395
Patent No. 6359197

GENERAL INFORMATION:
APPLICANT: Amasino, Richard M
APPLICANT: No. 6359197, Yoo-Sun
TITLE OF INVENTION: Transgenic Plants with Altered
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,395
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.94908
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-971-395-1

Query Match 28.6%; Score 549.2; DB 3; Length 3182;

Best Local Similarity 83.5%; Pred. No. 1.3e-153;
Matches 623; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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QY 682 CAAGACCGATGATCTACGTCTAATTTTCGGTCCAACTTGACAGAGAAAGCATGACTG 741
Db 2173 CTAAACACATGACCTGATCTAATTTTCGGTCCAACTTGACAGAGAAAGCATGACTG 2232
QY 742 CGATAGCTCTTGGCCAGACAGTGGCTCCCAATCTCTGCTGATCGGCTCCAAATGCT 801
Db 2233 CGATAGCTCTTGGCCAGACAGTGGCTCCCAATCTCTGCTGATCGGCTCCAAATGCT 2292
QY 802 GTCTCAACTATCAACCGGAGCGGGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTC 861
Db 2293 GTCTCAACTATCAACCGGAGCGGGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTC 2352
QY 862 GTCTGACCTTATGATGATCGCCCTTGTGTAAGGGTATCATTAACGCCAAGCACTCATG 921
Db 2353 GTCTGACCTTATGATGATCGCCCTTGTGTAAGGGTATCATTAACGCCAAGCACTCATG 2412
QY 922 AACGGCTCATTTGCGAGGTGCAATCAATCAAGGCCAAAGCGGGCTTATTCTTGAAGGAG 981
Db 2413 AATAGGCTGATCGAGAGGTGTATATATCATGAGGCCAACGGCGGCTTATTCTTGAAGGAG 2472
QY 982 GATCTATCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1041
Db 2473 GATCTATCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2532
QY 1042 GGCATATATTTTCGCAACAGATTTAGACAGAGAGAGCTTATGATGATGATGATGATGATG 1101
Db 2533 GGCATATATTTTCGCAACAGATTTAGACAGAGAGAGCTTATGATGATGATGATGATGATG 2592
QY 1102 GAGTTAAGCAGATGTTACGCCCCCTCTGCAAGCTCTTTCTATTATTCAGAGTTGGTTCAAC 1161
Db 2593 GAGTTAAGCAGATGTTACGCCCCCTCTGCAAGCTCTTTCTATTATTCAGAGTTGGTTATC 2652
QY 1162 TTTGGAGGAGAGCTCGCTGAGAGCCCATATCTGAAAGGATGATGATGATGATGATGATG 1221
Db 2653 TTTGGAGATGAACCTCGCTGAGAGCCCATATCTGAAAGGATGATGATGATGATGATGATG 2712
QY 1222 TGCTATTTGCTACCCAGAACAGATCAAGCCGATATGCTATTGACGCTCGACGCAATTA 1281
Db 2713 TGTTGTTTGTAGCCAGAACAGATCAAGCCGATATGCTATTGACGCTTGAACGCAATTA 2772
QY 1282 TGGAGATTAATTTGATTCACGATATGCTCAGAGTTTCTAATCATTCGCGCTGACAGAG 1341
Db 2773 TGGAGGTAAAGTTGATTAATGAGATGCTCAGAGATTTTCAATCATTCGCGCTGACAGAG 2832
QY 1342 AACGAAATTCCTTTGGTGGGCGGACAGCTGTGAAAGCGTTTGAAGAACCAACATTTTC 1401
Db 2833 AACGAAATTCCTTTGGTGGGCGGACAGCTGTGAAAGCGTTTGAAGAACCAACATTTTC 2892
QY 1402 GAATGTGATGATTTGACACCAAGTTTGG 1427
Db 2893 GAATGTGATGATTTGACACCAAGTTTGG 2918
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RESULT 8
US-08-413-135-1

Sequence 1, Application us/08413135

Patent No. 5689042

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M

APPLICANT: Gan, Shuhang

TITLE OF INVENTION: Transgenic Plants with Altered

TITLE OF INVENTION: Senescence Characteristics

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESS: Charles & Brady

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53703

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/413,135

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296,92808

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3183 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "SAG12-1 Promoter DNA"

US-08-413-135-1

Query Match 28.5%; Score 546.6; DB 2; Length 3183;
Best Local Similarity 82.4%; Pred. No. 7.9e-153;
Matches 627; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

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QY 667 GTATTCAACATATGCAAGACCGATGGATCTACGCTAATTTTGGTCCAACTTGACAG 726
Db 2159 GTCTATTTAATCTTCTTAAACATGAGACCTGACATCTAATTTTGGTCCAACTTGACAG 2218
QY 727 GAAAGACATGACATGACATAGCTCTTCCAGACAGACTGCGCTCCAGTCTCGCTCG 786
Db 2219 GAAAGACATGACATGACATAGCTCTTCCAGACAGAGAGGCTTCCAGTCTCGCTCGCTCG 2278
QY 787 ATGCGCTTCAATGCTGCTCTCACTAATCAACCGGAGCGGCGCAACAGTGAAGAAC 846
Db 2279 ATGCGCTTCAATGCTGCTCTCACTAATCAACCGGAGCGGAGCGGCGCAACAGTGAAGAAC 2338
QY 847 TGAAGAGACAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
Db 2339 TGAAGAGACAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2398
QY 907 CCAAGACAGCTCATGAACGGCTCATTTGCGGAGGTGCACAATCAGAGGCCCAAGCGCGGC 966
Db 2399 CCAAGACAGCTCATGAACGGCTCATTTGCGGAGGTGCACAATCAGAGGCCCAAGCGCGGC 2458
QY 967 TTATTTCTTGAAGAGATCTATCTGCTGCTCAGAGTGCATGAGGCGCAAAAGTCTTATTTGA 1026
Db 2459 TTATTTCTTGAAGAGATCTATCTGCTGCTCAGAGTGCATGAGGCGCGCAAAAGTCTTATTTGA 2518
QY 1027 ACGGGATTTTGTGTTGATATTAATTCGCAACGAGTTAGACAGAGAGAGGTTTATTTGA 1086
Db 2519 GTGAGATTTTGTGTTGATATTAATTCGCAACGAGTTAGACAGAGAGAGGTTTATTTGA 2578
QY 1087 GCGTGGCCAGACAGAGTTAAGCAGATTTACGCCCCCTCTGACAGTCTTTTCTATTATTC 1146
Db 2579 AAGGGGCCAAGCCAGAGTTAAGCAGATTTACGCCCCCTCTGACAGTCTTTTCTATTATTC 2638
QY 1147 AAGAGTTGTTCAACTTTGAGAGGAGCTCGGCTGAGAGGCCCAATCTGAAGAGATTCATG 1206
Db 2639 AAGAGTTGTTTATCTTTGAGATGAACCTCGGCTGAGAGGCCCAATCTGAAAGATTCATG 2698
QY 1207 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1266
Db 2699 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2758
QY 1267 AGCTGACGACATATGAGAGATTAATTTGATTCAGGATGCTCAGAGATTTCTAATTC 1326
Db 2759 AGCTGACGACATATGAGAGATTAATTTGATTTAATTTGATGATGATGATGATGATGATGATG 2818
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QY 1327 ATCCGGTGCAGACGAAACGAATTCCTTTGGTGGCGCGACAGCTTGTCAAGCCTTTG 1386
DB 2819 ATGCGCGCCACAGAGAAAGAAATTCGCCAAGTTAACGACGCGCTTTGACGAGATCG 2878
QY 1387 AAGGACCAACATTTGATGTAGATTGACACAGTTTGG 1427
DB 2879 AAGGTATCCGTTCCGAAATGTATTAGGTTAACGCCAGCCTG 2919

RESULT 9
US-09-434-837-12
; Sequence 12, Application US/09434837
; Patent No. 6759574
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/09/434,837
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 60/107,185
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-434-837-12

Query Match 28.4%; Score 545.4; DB 3; Length 723;
Best Local Similarity 84.6%; Pred. No. 7.9e-153;
Matches 612; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTCTAATTTTGGTCCAACTTGCACAGGAAACATTCAGCTGCGATAGCT 749
DB 1 ATGACCTGCACTTAATTTTGGTCCAACTTGCACAGGAAACATTCAGCTGCGATAGCT 60
QY 750 CTGCGCCAGCAGACGTGGCTCCCAAGTCTCTGCTGATCGCGTCCAAAGTCTGCTCA 809
DB 61 CTGCGCCAGCAGACGTGGCTCCCAAGTCTCTGCTGATCGCGTCCAAAGTCTGCTCA 120
QY 810 CTATTAACCGGAAGGCGCGACCAACATGTGAAAGAACTGAAAGCACTGCTGTGAC 869
DB 121 CTATTAACCGGAAGGCGCGACCAACATGTGAAAGAACTGAAAGCACTGCTGTGAC 180
QY 870 CTGATGATCGCCCTTTGGTAAAGGTTATCATTAAGCCAGCAAGCTCATGAAGGCTC 929
DB 181 CTGATGATCGCCCTTTGGTAAAGGTTATCATTAAGCCAGCAAGCTCATGAAGGCTC 240
QY 930 ATTGCGAGGTGCACATCAAGGCGCGGCTTATTTGAGGAGATCTATC 989
DB 241 ATCGAGAGGTGTATATCATGAGGCCAAGCGGCTTATTTGAGGAGATCTATC 300
QY 990 TCGTTGCTCAGGTGATGCGCAAGTGTATTGAAACGCGGATTTTGTGGCATATT 1049
DB 301 TCGTTGCTCAGGTGATGCGCAAGTGTATTGAAACGCGGATTTTGTGGCATATT 360
QY 1050 ATTGCGAGGTGCACATCAAGGCGCGGCTTATTTGAGGAGATCTATC 1109
DB 361 ATTGCGAGGTGCACATCAAGGCGCGGCTTATTTGAGGAGATCTATC 420
QY 1110 CAGATGTTAGCCCTCTGCAAGTCTTCTATTATCAAGAGTTGTTCACTTTGAGG 1169
DB 421 CAGATGTTAGCCCTCTGCAAGTCTTCTATTATCAAGAGTTGTTATCTTTGAGAT 480
QY 1170 GAGCTCGGCTGAGGCGCAATCTGAAAGGATCGATGATATCGATATGCCCTGTATT 1229
DB 481 GAGCTCGGCTGAGGCGCAATCTGAAAGGATCGATGATATCGATATGCCCTGTATT 540
QY 1230 GCTACCCGAGAACGATCAAGCGCGGATGATGATGATGATGATGATGATGATGAT 1289

DB 541 GCTACCCGAGAACGATCAAGCGCGGATGATGATGATGATGATGATGATGATGAT 600
QY 1290 AAATTGATTCAGCGTATGCTTCAGAGATTTTCAATCAATGCGCTGACAGGAAAGAAA 1349
DB 601 AAGTTGATTAATGAGATGCTCAGAGATTTTCAATCAATGCGCGCAACAGGAAAGAAA 660
QY 1350 TTCCCTTTGGTGGGCGCAGAGCTGTGAAAGGCTTTGAAAGCAACATTTGAAATGCA 1409
DB 661 TTCCCTTTGGTGGGCGCAGAGCTGTGAAAGGCTTTGAAAGGCTTTGAAATGCA 720
QY 1410 TAG 1412
DB 721 TAG 723

RESULT 10
US-09-434-837-5
; Sequence 5, Application US/09434837
; Patent No. 6759574
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/09/434,837
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 60/107,185
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-434-837-5

Query Match 28.1%; Score 539.4; DB 3; Length 747;
Best Local Similarity 84.5%; Pred. No. 5.1e-151;
Matches 606; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 696 CTAGCTTAATTTTGGTCCAACTTGCACAGGAAACATTCAGCTGCGATAGCTTCTGCC 755
DB 18 CTGAATCTTAATTTTGGTCCAACTTGCACAGGAAACATTCAGCTGCGATAGCTTCTGCC 77
QY 756 CAGCAGACTGCGCTCCCAAGTCTCTGCTGATCGCGTCCAAAGTCTGCTCAACTATCA 815
DB 78 CAGCAGACTGCGCTCCCAAGTCTCTGCTGATCGCGTCCAAAGTCTGCTCAACTATCA 137
QY 816 ACCGGAAGCGGCGCAACATGTGAAAGAACTGAAAGCAAGCTGCTGTGATCTTGAAT 875
DB 138 ACCGGAAGCGGCGCAACATGTGAAAGAACTGAAAGCAAGCTGCTGTGATCTTGAAT 197
QY 876 GATGCGCTTTGGTAAAGGTTATCATTAAGCCAGCAAGCTCATGAAGGCTCATTCG 935
DB 198 GATGCGCTTTGGTAAAGGTTATCATTAAGCCAGCAAGCTCATGAAGGCTCATTCG 257
QY 936 GAGGTGCAATCAAGGCGCGGCTTATTTGAGGAGATCTATCTGTTG 995
DB 258 GAGGTGTAATATCAAGGCGCGGCTTATTTGAGGAGATCTATCTGTTG 317
QY 996 CTCAGGTGATGCGCAAGTGTATTGAAACGCGGATTTTGTGGCATATTATTCGC 1055
DB 318 CTCAGGTGATGCGCAAGTGTATTGAAACGCGGATTTTGTGGCATATTATTCGC 377
QY 1056 AAGAGTTAGCAGCAGAGAGCTTATGAGCGTGGCCAAAGCAAGTTAAACAGATG 1115
DB 378 CACAAGTTAGCAGCAGAGAGCTTATGAGCGTGGCCAAAGCAAGTTAAACAGATG 437
QY 1116 TTACGCCCTCTGCAAGTCTTCTATTATCAAGAGTTGTTCACTTTGAGGAGATCT 1175
DB 438 TTGACCCCGCTGAGGCGCAATCTGAAAGGATCGATGATATCGATATGCCCTGTATT 497
QY 1176 CGGCTGAGGCGCAATCTGAAAGGATCGATGATATCGATATGCCCTGTATTGTTGCTAAC 1235

Db 498 CGGCTGAGGCCCATTTCTGAAGAGATCGATGGATATTCGATATGCCATGTTTGGCTAGC 557
 QY 1236 CAGAACCAAGATCAACGCCCGATATGCTATTTGACGTCGACGAGATATGGAATAAATTG 1295
 Db 558 CAGAACCAAGATCAACGCCCGATATGCTATTTGACGTCGACGAGATATGGAAGTAAGTTG 617
 QY 1296 ATTCAACGGTATCGCTCAGAGATTTCTAATCCATGCGCGTCGACAGGAAACAGAAAATTCCT 1355
 Db 618 ATTATATGGAGATCGCTCAGAGATATTTCAATCCATGCGCGCAACAGGAACAATAATTCCT 677
 QY 1356 TTGGTGGGCGGACGCTGTGAAACGTTTGAAGACCAACATTTGCAATGTGATAG 1412
 Db 678 CAAGTTAACGACGCCCTTTGACGAGATTCGAAGTCAATCCGTTTCGAAATGTATTAAG 734

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RESULT 11
US-09-434-837-9
: Sequence 9, Application US/09434837
: Patent No. 6759574
: GENERAL INFORMATION:
: APPLICANT: Ream, Walt et al.
: TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
: TITLE OF INVENTION: Methods and Compositions for Producing the Same
: FILE REFERENCE: 53629
: CURRENT APPLICATION NUMBER: US/09/434,837
: EARLIER FILING DATE: 1999-11-04
: EARLIER APPLICATION NUMBER: 60/107,185
: EARLIER FILING DATE: 1998-11-05
: NUMBER OF SEQ. ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO 9
: LENGTH: 2544
: TYPE: DNA
: ORGANISM: Agrobacterium tumefaciens
: US-09-434-837-9

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Query Match	Similarity	15.9%	Score 305.4	DB 3	Length 2544
Best Local	Similarity	81.4%	Pred. No. 1,4e-80		
Matches	354	Conservative	0	Mismatches	81
				Indels	0
				Gaps	0
QY	978	GGAGGATCTATCTCGTTGCTGCTAGGTGCATGGCGCAAGTCGTTATTGGAAAGCGGATTTT	1037		
Db	2097	GCAGATCTACACCTCGTTGCTCAACTGCATGGCGGCAACAGCTATTGGAGTGCAGATTTT	2156		
QY	1038	CGTTGGCATATTATTCCGACAGAGTTAGCAGACGAGAGAGCTTATGAGCGTGGCCAA	1097		
Db	2157	CGTTGGCATATTATTCCGACAGAGTTAGCAGACGAGAGAGCTTATGAGAGCGGCCAA	2216		
QY	1098	ACCAGAGTTAAGCAGATGTTACGCCCTCTGTGAGGTCTTTCTATTATCCAAAGTTGGTT	1157		
Db	2217	GCCAGAGTTAAGCAGATGTTGACCCCTGTGAGGCGCATTTCTATTATCAAGAGTTGGTT	2276		
QY	1158	CAACTTTGAGAGGAGACCTCGGTGAGGCCCATCTGGAAGGATGCATGATATGATAT	121		
Db	2277	TATCTTTGGATGAACCTCGGTGAGGCCCATCTGGAAGGATGCATGATATGATAT	233		
QY	1218	GCCCTGCTATTGTTGCTACCCAGAACAGATCACGCCCGATATGCTATTGCAAGCTGACGCA	1277		
Db	2337	GCCATGTTGTTGTTGCTAGCCAGAACAGATCACGCCGATATGCTATTGCAAGCTTACGCCA	2396		
QY	1278	GATATGAGGAATTAATTGATTCACGCGTATCGCTGAGAGTTTCTATCCATCCGCGGTGGA	1337		
Db	2337	AATATGGAAGGTAAAGTTGATTTATGATGATCGCTGAGAGTATTTATTCATACGCGGCCAA	2455		
QY	1338	CAGGAACGAATAATCCCTTTGGTGGCGCGCACAGCTGTGCAAGCGTTTGAAGACCAACA	1397		
Db	2457	CAGGAACGAATAATCCCCCAAGTTAAGCAGCGCGCTTTCGACGAGATTGGAAGGTATCCG	2516		
QY	1398	TTTGCATATGTGATAG 1412			
Db	2517	TTGGAATGTATTAG 2531			

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1 RESULT 12
2 US-08-054-985-2
3 Sequence 2, Application US/08054985
4 Patent No. 5496732
5 GENERAL INFORMATION:
6 APPLICANT: Smigocki, Ann C
7 APPLICANT: Neal Jr, John W
8 TITLE OF INVENTION: ENHANCED INSECT RESISTANCE IN PLANTS
9 TITLE OF INVENTION: GENETICALLY ENGINEERED WITH A PLANT HORMONE GENE
10 TITLE OF INVENTION: INVOLVED
11 TITLE OF INVENTION: IN CYTOKININ BIOSYNTHESIS
12 NUMBER OF SEQUENCES: 3
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Janelle S. Graeter
15 STREET: Room 411, Building 005, BARC-W
16 CITY: Beltsville
17 STATE: Maryland
18 COUNTRY: United States of America
19 ZIP: 20705
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: Patent in Release #1.0, Version #1.25
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/054,985
27 FILING DATE: 30-APR-1993
28 CLASSIFICATION: 800
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Graeter, Janelle S
31 REGISTRATION NUMBER: 35024
32 REFERENCE/DOCKET NUMBER: 0175.92
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (301) 504-6629
35 TELEFAX: (301) 504-5060
36 INFORMATION FOR SEQ ID NO: 2:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 584 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: DNA (genomic)
43 HYPOTHEITICAL: NO
44 ANTI-SENSE: NO
45 ORIGINAL SOURCE:
46 ORGANISM: Agrobacterium tumefaciens
47 US-08-054-985-2

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	Query Match	Score	DB 2	Length	584
	Best Local Similarity	70.6%	Pred. No.	1.1e-58	
Matches	479	Conservative	0	Mismatches	78
				Indels	121
				Gaps	8
QY	630	ATGATCTACGCTCTAATTTTGGCTCCACTTGCACAGAAAGACATCGACTCGATGAGCT	749		
DB	1	ATGGACCTGCATCTAATTTTGGCTAATTGCACAGAAAGACAGACACCGGATAGCT	60		
QY	750	CTTGGCCAGCAGACTGGCTCCGAGTCCCTGCTCGATCGGCTCCATGCTGTCTCAA	809		
DB	61	CTTGGCCAGCAGACTGGGCT-----GGATCCAAATGCTGTCTCTCAA	100		
QY	810	CTATCAACCGGAAGCGGGCGACCAACAGTGAAGAACTGAAGGAACGACTGCTGTATC	869		
DB	101	CTATCAACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGGAACGACGCTCTCTAC	160		
QY	870	CTTGATGATCGCCCTTTGGTAAAGGATCATTAACGCCAGCAAGCTCATGACGGCTC	929		
DB	161	-----GGAGGGTATCATCGCAGCCAAACCAAGCTCATATAGGCTG	200		
QY	930	ATTGGGAGGTGACCAATCAACGAGGCCAAAGCGGGCTTATCTTGAGGAGAGATCTATC	989		
DB	201	ATCGAGGAGGTATATATCATATGAGCCAAAGCGGGCTTA-----	240		


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QY 990 TCGTTCAGAGTCGATGCGCAAGTGTATTGGAACGGGATTTTGTTCGATATT 1049
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Db 241 TCGTTCAGAGTCGATGCGCGGAAAGAGCTATTGGAAGCGAGATTTTGTTCGATATT 300
|||
QY 1050 ATTGCAACGAGTTGACAGAGAGAGAGCTTCATGAGCGTGGCAAGACAGAGTTAAG 1109
|||
Db 301 ATTGCGCACAGTTACCGGAC-----GGCCAAAGCGCAGAGTTAAG 340
|||
QY 1110 -CAGATGTTACGCGCCCTGACAGTCTTTCTATTATTCAGAGAGTTGTTCACTTTGAG 1168
|||
Db 341 CCAGATGTTGACCGCCCTGACAGGCGCATTCATTATTC-AGAGTTGTTTATCTTTGGA 399
|||
QY 1169 GAGCGCTGGCTGAGCGCCATCTGGAAGGATCGATGATTCGATATGCCCTGCTATT 1228
|||
Db 400 T-----TTCTAAAGAGATCGATGATTCGATATGCCATGTTGTT 440
|||
QY 1229 TGCTACCCAGAACGAGATCAGCGCGGATATGCTATTGACGCTCGACGAGATATGAGA 1288
|||
Db 441 TGCTACCCAGAACGAGATCAGCGCGGATATGCTATTGAG----- 480
|||
QY 1289 TAAATGATTCAGCGTATCGCTCAGAGAGTTTCTAAATCCATGCGCGTCGACAGAACAGA 1348
|||
Db 481 TAAATGATTCAGCGTATCGCTCAGAGAGTTTCTAAATCCATGCGCGTCGACAGAACAGA 540
|||
QY 1349 ATTCCTTTGTTGGGCGC 1366
|||
Db 541 ATTCCTTTGTTGGGCGC 558
|||
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RESULT 13

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US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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Query Match 2.3%; Score 44.8; DB 3; Length 832;

Best Local Similarity 12.3%; Pred. No. 0.0097; Matches 37; Conservative 138; Mismatches 125; Indels 0; Gaps 0;

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QY 1423 TTTTGTTCAGAGTCGCTATTGTAATGATGATGCTTCTTTGTTGTTGTTGTTGTT 1482
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Db 16 WTKKMSWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 75
|||
QY 1483 TGTGATAGAGCAAGTGTGTTGAAACTTTTCTAGCTGTTATTTTCACTCTCTGGAC 1542
|||
Db 76 TKTKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 135
|||
QY 1543 GATGTTTACAATATATATATGTAATGTAATGTTGTTTATATTCGTGAAGCAATATA 1602
|||
Db 136 YSSGKMTWKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 195
|||
QY 1603 TGTGATAGATAGCGGTTATCAAAATTTGACAAAATTTGTAAGGTTCTTTATGCGG 1662
|||
Db 196 WRKRSYSASAKRCVSCGWMAMSMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 255
|||
QY 1663 AGTTTGTGACTTTTTCATCATTTGTCGCTAAGAGAGTTACGATATCCATACTGTA 1722
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Db 256 KSKTSYKSMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 315
|||
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RESULT 14

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US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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Query Match 2.2%; Score 43; DB 3; Length 832;

Best Local Similarity 10.2%; Pred. No. 0.033; Matches 37; Conservative 167; Mismatches 157; Indels 0; Gaps 0;

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QY 6 CCGTTACAGATTCAGAGTTCGTAATTCATATTAATGCAATCTGATGTTTAATA 65
|||
Db 362 YTTTMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 303
|||
QY 66 CGAATGATATGCGGTTAAGAAATGATTTTATTTATTTATTTTCACTATGTTGAAGT 125
|||
Db 302 STRWYCMWCMKCMYRCRCAMWRCMWSYAMGKMSRMSAMSMCTRYKKGGTYW 243
|||
QY 126 TGCAATATATGCTAATGTAATTAATAAATTAATGCTACCGCATTTGTTCAATGCG 185
|||
Db 242 TMKCTCATWCMYKKYKKWMSKTCWSSRGVITSTSTSYMMWMMWMMWMMWMMWMM 183
|||
QY 186 GCCGTTATTTCAAAATATCTTTGATTTTGTACAGAGCAAGCTGACAGAAATAAT 245
|||
Db 182 WMSYTWYAMGCKMMWRYATTWBRAMMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 123
|||
QY 246 AAAAGACGCTGTTGTTAAGAAATGCTATCATATGTCGCCAGCTATAGGCCATTAA 305
|||
Db 122 YRYWRRKKSRYRTCAWAAYAKTYSYWCWRRWKKCKMMWMMWMMWMMWMMWMMWMM 63
|||
QY 306 TCAATTTGAAATATGCGCGCCCTTATTTTGAAGCTCATCAATCAATATTAATAAAT 365
|||
Db 62 RYWRMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMM 3
|||
QY 366 C 366
|||
Db 2 Y 2
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RESULT 15

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US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 18:36:54 ; Search time 8253 Seconds
(without alignments)
13002.447 Million cell updates/sec

Title: US-10-817-483-1

Perfect score: 1919

Sequence: 1 ggatccgcgtacaaagtctg.....tacgcattatagaagaacct 1919

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 48236798 segs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

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2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_hnc:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gsa1:*

12: gb_gsa2:*

13: gb_gsa3:*

14: gb_gsa4:*

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	55.2	2.9	1099	14	CNS06PYL
2	54.2	2.8	1101	14	CNS016TA
3	52	2.7	754	11	BH483858
4	52	2.7	786	11	BH445413
5	52	2.7	796	11	BH514721
6	51	2.7	1380	12	CC190214
7	51	2.7	1489	14	AG350139
8	50.8	2.6	859	14	CNS00KTL
9	50.6	2.6	742	11	BZ390485
10	50.6	2.6	1101	14	CNS017JM
11	49.4	2.6	813	3	BME57710
12	49.4	2.6	878	14	CNS0187R
13	49.2	2.6	1250	12	CI048827
14	49	2.6	292	2	B1742580
15	49	2.6	1203	14	CNS015WU
16	48.8	2.5	1300	7	BE420576
17	48.6	2.5	876	13	CZ529924
18	48.6	2.5	1078	12	CI031456
19	48.6	2.5	1201	14	CNS016E1

20	48.4	2.5	1097	12	CI024868
21	48.2	2.5	881	11	AZ681832
22	48.2	2.5	1084	14	CNS0025S
23	48	2.5	1201	14	CNS016DB
24	47.8	2.5	322	14	DE042918
25	47.8	2.5	938	14	CNS006TJ
26	47.4	2.5	867	14	CNS00CX5
27	47.4	2.5	1371	9	DN662120
28	47.2	2.5	500	1	AU087545
29	47.2	2.5	500	3	BP114521
30	47.2	2.5	639	13	CW330724
31	47.2	2.5	732	13	CM439569
32	47.2	2.5	942	3	BQ930773
33	47	2.4	389	9	DN197640
34	47	2.4	819	13	CZ536319
35	47	2.4	1184	14	CNS04P4P
36	46.8	2.4	546	3	BM620921
37	46.8	2.4	665	3	BM634198
38	46.8	2.4	826	13	DU068950
39	46.8	2.4	839	13	CZ536111
40	46.8	2.4	1225	14	CNS0161D
41	46.6	2.4	695	3	BP513401
42	46.6	2.4	750	14	CNS011ID
43	46.6	2.4	796	14	CNS0118D
44	46.6	2.4	865	11	AZ693005
45	46.6	2.4	866	11	AZ672468

ALIGNMENTS

RESULT 1	CNS06PYL	1099 bp	DNA	linear	GSS 05-JUL-2001
LOCUS	T7 end of clone AM0A001B06 of library AM0A	from strain CLUB 89 of			
DEFINITION	Yarrowia lipolytica, genomic survey sequence.				
ACCESSION	AL409987				
VERSION	AL409987.1	GI:1217872			
KEYWORDS	GSS.				
SOURCE	Yarrowia lipolytica				
ORGANISM	Yarrowia lipolytica				
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
AUTHORS	Saccharomycetales; Dipodascaceae; Yarrowia.				
	1 (bases 1 to 1099)				
	Souci�t,J.L., Aigle,M., Artiguenave,F., Blandin,G.,				
	Botolint-Fukuhara,M., Bon,E., Broctier,P., Casaregola,S.,				
	de-Montigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B.,				
	Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Portier,S.,				
	Saurin,W., Tekala,F., Toffano-Nic�che,C., Wesolowski-Louvel,M.,				
	Wincker,P. and Weissenbach,J.				
	Genomic exploration of the hemiascomycetous yeasts: 1. A set of				
	Yeast species for molecular evolution studies				
	FEMS Lett. 487 (1), 95-100 (2000)				
	11152876				
JOURNAL	2 (bases 1 to 1099)				
PUBMED	Casaregola,S., Neuvéglise,C., Lepingle,A., Bon,E., Feyn�rol,C.,				
REFERENCE	Artiguenave,F., Wincker,P. and Galliardin,C.				
AUTHORS	Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia				
TITLE	lipolytica				
JOURNAL	FEMS Lett. 487 (1), 95-100 (2000)				
PUBMED	11152892				
REFERENCE	3 (bases 1 to 1099)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-SEP-2000) Genoscope - Centre National de S�quenc�age,				
COMMENT	2 rue Gaston Cr�mieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :				
	seq@genoscope.cns.fr - Web : www.genoscope.cns.fr)				
	This GSS is part of a random genomic sequencing program of thirteen				
	yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces				
	exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,				
	Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces				
	lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia				
	angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,				

Query Match 2.7%; Score 52; DB 11; Length 796;
 Best Local Similarity 53.4%; Pred. No. 0.044;
 Matches 109; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 79 GTAGAAATGATGATTTTATTTATTTATTTCTTCACTATGTTGAAGTTGCATATATGC 138
 DB 280 GCATACAAATGTTTATTTATTTATTTATTTAAATCTTAATTAACATGATTGAAATATTA 339
 QY 139 TAATGTAATAATTTAAAAATTAATGATGCGCATTGTTCAATGGCCGTTATTTCAA 198
 DB 340 TACAGCTAATTAATAAAGTATTAATGACATTAATTAATAAATATTTAATTTTAAAGTA 399
 QY 199 AAATATCTTATTTTGTAGAGACACACACGACAGAGTAATAAAGACGCGTT 258
 DB 400 AGAATATTTTGAATTTTCTTCAACAGATTTTTCGAATTAATAAATAAAGACAGTT 459
 QY 259 GTTAAGAAATGCTATCATATGTG 282
 DB 460 TTATAGATGAATTTTATATGTG 483

RESULT 6
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 LOCUS CH261-3712_RM1.1 CH261 Gallus gallus genomic clone CH261-3712,
 DEFINITION genomic survey sequence.
 ACCESSION CCI90214
 VERSION CCI90214.1 GI:30435240
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianine; Gallus.
 1 (bases 1 to 1380)
 Kremiczki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Wards, E. and Wilson, R.
 Gallus gallus BAC End Reads
 Unpublished (2003)
 CONTACT: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.wustl.edu
 Insert Length: 182000 Std Error: 0.00
 Seq primer: RM1 TACGACTCATATAGGGAGA
 Class: BAC ends
 High quality sequence start: 266
 High quality sequence stop: 809.
 Location/Qualifiers
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 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CH261 Female Chicken library - For library and clone
 ordering information: http://www.chori.org/bacpac"

ORIGIN
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 Best Local Similarity 47.3%; Pred. No. 0.089;
 Matches 167; Conservative 0; Mismatches 185; Indels 1; Gaps 1;

QY 16 TATGACAGCTTTTGAATTTGCAATTAATGAATCTGATGTTAATACGAATGTAAT 75
 DB 1006 TAGTCAAAATTTTAAATTTTAAATTTTAAATGTTTAAATTTTAAATTTTAAATTTGCTT 1065
 QY 76 GGCGTAGAAATATGATTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 134

DB 1066 TTTTAAATTTAAATAAATTTAATTTCTTTAAAAAAGTTAATTTGTTTAAACA 1125
 QY 135 ATGCTATGTAATAATTTAAATTTATTTACTGCCGATTTGTTCAATTTGCGCGTATTT 194
 DB 1126 AAAAAAATTTTCTTTAAAAATTTTAAAAATTTAATTTGTTCAAAAAGGTGGTTAAA 1185
 QY 195 TCAAAAATCTTTGATTTTGTTPACGAGCAACAGCTGACGAGTAATTAATAAGACGC 254
 DB 1186 TCAAAAACCTTTAATTTTAAAAAGGGTATTAATTTCCCTTAATTTTAAAAAANGT 1245
 QY 255 TGTGTTAGAAATTTGCTATCATATGTCGCCAGCTATAGGCCATTTAAGTTCAATTTGTG 314
 DB 1246 TTTTGTAATAATTTCAATTAATTTATTTCCNNTTTTTCACCATGANAATTAATTAATTTG 1305
 QY 315 AAATAGCGCCCTTATTTGACGCTCATCAATCAATTAATAAATATCT 367
 DB 1306 GAAAAAATTTTCAATTTGTTTTCAGNCANATTAATTAATTAATTTTCT 1358

RESULT 7
 AG350139 1489 bp DNA linear GSS 18-DEC-2004
 LOCUS Mus musculus molossinus DNA, clone:MSWg01-146K14.TJ, genomic survey
 DEFINITION sequence.
 ACCESSION AG350139
 VERSION AG350139.1 GI:47923449
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murine; Mus.
 1
 Abe, K., Noguchi, H., Tagawa, K., Yuzurika, M., Toyoda, A., Kojima, T.,
 Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and
 Shiroishi, T.
 Contribution of Asian mouse subspecies Mus musculus molossinus to
 genomic constitution of strain C57BL/6J, as defined by BAC-end
 sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)
 15574823
 2 (bases 1 to 1489)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 Direct Submission
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
 1-7-22 Saitama-shi, Tsukuba-shi, Ibaraki-shi, Yokohama-shi, Kanagawa-shi, Japan
 (E-mail: hattori@ipc.riken.jp, URL: http://hpg.gsc.riken.go.jp/,
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the mouse BAC library MSWg01. For BAC
 library availability, please contact Kuniya Abe (abe@ipc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@ipc.riken.jp
 PRIMERS
 Sequencing : TJ
 LIBRARY : PBACE3.6
 Vector : EcoRI
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
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ORIGIN

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isolated from early log phase trophozoites of E. invadens

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QY 139 TAATGTAATAATTAATGATGCGCATTTGTCGAATGGCGCGTATTTCAA 198
DB 449 TTTATTTATTTATTTAAATTAATTAATTAATTTTATTTTAAAGTCATCCCTTAA 390
QY 199 AATATCTTTGATTTTGTACGAGCAACGACGAGAGTAATTAAGAGCGCTGT 258
DB 389 AATATCTTTATTTATTTATTAATTAATTAATTAATTAATTAATTAATTAAGCTAAA 330
QY 259 GTTAAGAAATGTGATCATATGCGCAGCTATAGGCCATTAACTTCAATTTGAAAT 318
DB 329 TTAATATCTTTCTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTTCTAA 270
QY 319 AGCGCGCTTATTTGACGCTCATCAATCAATTAATTAATTAATTAATTAATTAATTCACCTCGG 378
DB 269 TACATATTTAAATGATTTTCCACATTAATCTTTTATTAATTAATTAATTTTAAATTC 210
QY 379 CAGCAATGATGTAATTA 395
DB 209 GAGAAAAATTAATTAATA 193
RESULT 12
LOCUS CNS0187R/c 878 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
BACH04E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL108993.1 GI:5629297
VERSION GSS.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 878)
Genoscope.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : segreif@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES
source Location/Qualifiers
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Best Local Similarity 25.2%; Pred. No. 0.22;
Matches 80; Conservative 93; Mismatches 144; Indels 0; Gaps 0;
QY 1397 ATTTGGAATGATGATGACACAGTTTGTTCGACTTGCTATTTGAATGAAT 1456
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QY 1457 GTTCGTTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1516
DB 275 TTKMKMTGTYTK 216
QY 1517 ACTGTTATTTTCACTCTCTTGACGATGTTTACAAATATTAATTTGTGAATTTG 1576

DB 215 WWWWCTTWWWWWTTTKWWTTTAAATKWWTTAAATKWWTTAAATCAKAYATTCAGKCAAGW 156
QY 1577 GTTTATTAATTCGTAGAAGCAATTAATGTAATAGCCGTTATCAAAATTTAGCAAAA 1636
DB 155 KWWTTTTTTTWWTTKKKKCYTKKKKWWTCMGCMTWTCYTKTMMTTTTTTTCKWTKT 96
QY 1637 ATTTGTAAGGTTCTTTATTTATGGGTGAGGTGTGCACTTTTCATCTTTGCGGTAA 1696
DB 95 TWTWTTTTTKMKKTTTTTTTTTTTGTGKWWTTTTTTTTCATATWTTGTATTTTTCAYW 36
QY 1697 GTTACGATATTCATTA 1713
DB 35 TTTACGAGACACCAATTA 19
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DEFINITION CH216-68N9_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-68N9,
genomic survey sequence.
ACCESSION CL048827
VERSION CL048827.1 GI:40504740
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1250)
Krenitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCATATAGGGAGA
Class: BAC ends
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High quality sequence stop: 611.
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BAC library"
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Best Local Similarity 51.9%; Pred. No. 0.26;
Matches 111; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
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QY 1460 CGTTCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1519
DB 958 CTCTTTTAATATGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 899
QY 1520 GGTATATTTTCACTCTCTTGACGATGTTTACAAATATTAATTTGTGAATTTGTGTT 1579
DB 898 ATTTTGTGAGTTAAATTTGACCAATTTTATTTTATTTTATTTAGGCAATTCATCC 839

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 19:20:37 ; Search time 2432 Seconds
(without alignments)
9695.712 Million cell updates/sec

Title: US-10-817-483-1

Perfect score: 1919

Sequence: 1 ggatccgcgtacacagctg.....taagcattacagacagctt 1919

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1919	100.0	1919	9	US-10-817-483-1
2	1089.8	56.8	1997	8	US-10-465-008-1
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5	720.4	37.5	2722	13	US-11-139-461-8
6	720.4	37.5	2722	13	US-11-139-461-9
7	720.4	37.5	5622	13	US-11-139-461-7
8	720	37.5	723	7	US-10-409-701-2
9	717	37.4	717	7	US-10-369-493-38935
10	583.8	30.4	723	9	US-10-821-711-2
11	583.6	30.4	720	9	US-10-369-493-35042
12	583.6	30.4	720	7	US-10-369-493-38138
13	582.2	30.3	723	16	US-11-156-084-1
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18	580.6	30.3	723	16	US-11-156-084-18	Sequence 18, Appl
19	578.8	30.2	720	7	US-10-369-493-38949	Sequence 38949, A
20	578.8	30.2	720	7	US-10-369-493-38953	Sequence 38953, A
21	578.8	30.2	720	7	US-10-369-493-38968	Sequence 38968, A
22	577.4	30.1	723	16	US-11-156-084-16	Sequence 16, Appl
23	577.2	30.1	2595	7	US-10-369-324-3	Sequence 3, Appl
24	577.2	30.1	2595	7	US-10-392-301-3	Sequence 3, Appl
25	577.2	30.1	2595	8	US-10-607-538-3	Sequence 3, Appl
26	577.2	30.1	2595	10	US-10-667-145-3	Sequence 3, Appl
27	577.2	30.1	2595	10	US-10-505-079-3	Sequence 3, Appl
28	577.2	30.1	9323	8	US-10-369-324-4	Sequence 4, Appl
29	577.2	30.1	9323	8	US-10-607-538-4	Sequence 4, Appl
30	577.2	30.1	9323	10	US-10-505-079-4	Sequence 4, Appl
31	554.4	28.9	777	7	US-10-369-493-38971	Sequence 38971, A
32	546.6	28.5	3183	15	US-10-072-077A-1	Sequence 1, Appl
33	546.6	28.5	3183	15	US-11-154-865-1	Sequence 12, Appl
34	545.4	28.4	723	6	US-10-187-339-12	Sequence 12, Appl
35	543.6	28.3	720	7	US-10-369-493-38936	Sequence 38936, A
36	543.6	28.3	720	7	US-10-369-493-38940	Sequence 38940, A
37	543.6	28.3	720	7	US-10-369-493-38964	Sequence 38964, A
38	543.6	28.3	720	7	US-10-369-493-38966	Sequence 38966, A
39	539.4	28.1	747	6	US-10-187-339-5	Sequence 5, Appl
40	503.8	26.3	11746	16	US-11-174-413-75	Sequence 75, Appl
41	503.8	26.3	11788	16	US-11-174-413-73	Sequence 73, Appl
42	503.8	26.3	11803	16	US-11-174-413-74	Sequence 74, Appl
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45	190.6	9.9	729	7	US-10-369-493-38941	Sequence 38941, A

ALIGNMENTS

RESULT 1
US-10-817-483-1
Sequence 1, Application US/10817483
Publication No. US20040237147A1
GENERAL INFORMATION:
APPLICANT: Habben, Jeffrey E.
APPLICANT: Zinselmeier, Christopher
APPLICANT: Tomes, Dwight
APPLICANT: Abbit, Shane
APPLICANT: Helenczaris, Timothy G.
TITLE OF INVENTION: Modulation of Cytokinin Activity in
TITLE OF INVENTION: Plants
FILE REFERENCE: 0803R
CURRENT APPLICATION NUMBER: US/10/817,483
CURRENT FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: US 60/460,718
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 09/545,334
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1919
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
FEATURE:
NAME/KEY: CDS
LOCATION: (690)...(1411)
OTHER INFORMATION: 1pt
US-10-817-483-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 721 GCACAGGAAGACATCGACTGAGTAGCTCTTGCCACAGACTGCGCTCCCAAGTCTCT 780
Qy 781 CGCTCGATCGCGTCCCAATGCTGTCTCAACTATCAACCGGAAAGCGGCGCAACAGTGG 840
Db 781 CGCTCGATCGCGTCCCAATGCTGTCTCAACTATCAACCGGAAAGCGGCGCAACAGTGG 840
Qy 841 AAGAACTGAAGGAACGACTGCTGTCTGTACCTTGATGATGCGCCTTTGGTAAAGGTTATCA 900
Db 841 AAGAACTGAAGGAACGACTGCTGTCTGTACCTTGATGATGCGCCTTTGGTAAAGGTTATCA 900
Qy 901 TTACAGCAAGCAAGCTCATGTAACGGCTCATTTGCGGAGGTGACAAATCAGAGGCGCAAG 960
Db 901 TTACAGCAAGCAAGCTCATGTAACGGCTCATTTGCGGAGGTGACAAATCAGAGGCGCAAG 960
Qy 961 GCGGCGTTATTTCTTGAGGAGAGATCTATCTCGTTGCTCAGGTGATGCGCGCAAGTGGTT 1020
Db 961 GCGGCGTTATTTCTTGAGGAGAGATCTATCTCGTTGCTCAGGTGATGCGCGCAAGTGGTT 1020
Qy 1021 ATTGGAAGCGGATTTTCTTGCGCTATATTTCCGAAGAAGTTTACACAGAGAGAGACT 1080
Db 1021 ATTGGAAGCGGATTTTCTTGCGCTATATTTCCGAAGAAGTTTACACAGAGAGAGACT 1080
Qy 1081 TCATGAGCGTGGCCCAAGACCAAGATTAAAGCAGATTTACGCCCTCTCTGACAGGTCTTTCTA 1140
Db 1081 TCATGAGCGTGGCCCAAGACCAAGATTAAAGCAGATTTACGCCCTCTCTGACAGGTCTTTCTA 1140

Qy 1141 TTATCAAGAGTGTGTTCAACTTTGAGGAGACCTCGGCTGAGGCCCATCTAGAGAGGA 1200
Db 1141 TTATCAAGAGTGTGTTCAACTTTGAGGAGACCTCGGCTGAGGCCCATCTAGAGAGGA 1200
Qy 1201 TCGATGATATCGATATGCGCCCTGCTATTTGCTACCCAGAACAGATCAGCGCCGATATGC 1260
Db 1201 TCGATGATATCGATATGCGCCCTGCTATTTGCTACCCAGAACAGATCAGCGCCGATATGC 1260
Qy 1261 TATTGAGCTCGACGAGATATGGAATTAATGATTCAACGATGATGCTCAGAGATTTC 1320
Db 1261 TATTGAGCTCGACGAGATATGGAATTAATGATTCAACGATGATGCTCAGAGATTTC 1320
Qy 1321 TAAATTCATGCGCGCTGACAGGAACAGAAATTTCCCTTTGCTGCGGCGCAGCTCTGCAAG 1380
Db 1321 TAAATTCATGCGCGCTGACAGGAACAGAAATTTCCCTTTGCTGCGGCGCAGCTCTGCAAG 1380
Qy 1381 CGTTGAAGGACCACTTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 CGTTGAAGGACCACTTTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 1441 GCTATTTGAATTAAGATGTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
Db 1441 GCTATTTGAATTAAGATGTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
Qy 1501 TTTGAAACTGTTTCTTCTGCTTATTTTCACTCTCTTGAAGCATGTTTCAAAATATTA 1560
Db 1501 TTTGAAACTGTTTCTTCTGCTTATTTTCACTCTCTTGAAGCATGTTTCAAAATATTA 1560
Qy 1561 TATTGTGAAATTTGTTGTTTATATTTGTTGTAAGAAAGAAATTAATGTTAAGTAAAGTAAAG 1620
Db 1561 TATTGTGAAATTTGTTGTTTATATTTGTTGTAAGAAAGAAATTAATGTTAAGTAAAGTAAAG 1620
Qy 1621 TCAAAATTTAGCAAAAATTTGTTAAAGTCTTTTATGCGGTGAGCTGTTGCACTTTTCAT 1680
Db 1621 TCAAAATTTAGCAAAAATTTGTTAAAGTCTTTTATGCGGTGAGCTGTTGCACTTTTCAT 1680
Qy 1681 CATTGTGCGGTGAAGAGTATGAGATATTCATATCTGTAATAAAACCCCGCAGAAATTTACGGG 1740
Db 1681 CATTGTGCGGTGAAGAGTATGAGATATTCATATCTGTAATAAAACCCCGCAGAAATTTACGGG 1740
Qy 1741 TGTGTCATTTAGTTGCGGTCAACATGATTTTGGCAATAGTGTGTAACCAAGCACTAGC 1800
Db 1741 TGTGTCATTTAGTTGCGGTCAACATGATTTTGGCAATAGTGTGTAACCAAGCACTAGC 1800
Qy 1801 CAACCGTTGATTAATCACTTAATGATGAAACGTTCACTTTCTTTGTTGAGCTGCTC 1860
Db 1801 CAACCGTTGATTAATCACTTAATGATGAAACGTTCACTTTCTTTGTTGAGCTGCTC 1860
Qy 1861 TTAGATGATGAGCTCGCTGCTGATTTTATTAACCGCGGGTTACGATTAATTAACAAGCTT 1919
Db 1861 TTAGATGATGAGCTCGCTGCTGATTTTATTAACCGCGGGTTACGATTAATTAACAAGCTT 1919

RESULT 2
US-10-465-008-1
; Sequence 1, Application US/10465008
; Publication No. US2004001616A1
; GENERAL INFORMATION:
; APPLICANT: MANKIN, LUKAS S.
; APPLICANT: DA COSTA E SILVA, OSMALDO
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING PLANT PERFORMANCE
; FILE REFERENCE: 16313-0232
; CURRENT APPLICATION NUMBER: US/10/465,008
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: 60/389,982
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1997
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens

US-10-465-008-1

Query Match 56.8%; Score 1089.8; DB 8; Length 1997;
Best Local Similarity 84.9%; Pred. No. 9.1e-271;
Matches 1270; Conservative 0; Mismatches 212; Indels 13; Gaps 4;

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2 GATCCGGTACAAAGTATGACAGTTTGTGAATTTGATATTAATGCAATCTGAGTGTTA 61
1 GATCCGTATCAAGTATGACAGTTTGTGAATTTGATATTAATGCAATCTGAGTGTTA 60
62 ATAAAGAAATGATAGGCGTA---GAATATGATATTTATTTGATTTATCTTCACTATG 117
61 ACAAGAAAGTATATGGCGTAAAGAAATTTGATTTGATTTGATTTGATTTGATTTG 120
118 TTGAAGTTGCAATATATGCTAATGTAAATTTAAATTTATGATGCGCGCATTTGTT 177
121 TTGAAGTTGCAATATATGAT-----GTATAGTAAATATATCACTGTCGCAATTATT 174
178 CAAATGGCGCGCTTATTTCAAAATATCTTTGATTTGTTAGAGAGACAGACCTGACAG 237
175 GAAATGGCACTGTATTTCAACCATATCTTTGATTTGATTTGATTTGATTTGATTTG 234
238 AAGTAAATATAAGACGCTGTTGTAAAGAAATGCTATCATATGCGCCAGTATAGGCGC 297
235 AAGTAAATATAAGACGCGCTGTTGTAAAGAAATGCTATCATATGCTGCTATATAGGAC 294
298 ATTATAGTTCAATTTGTGAATATGCGCGCTTATTTGATTTGATTTGATTTGATTTG 357
295 ATTATAG--TCAATTTGTGAATATGCTGCGCTTATTTGATTTGATTTGATTTGATTTG 353
358 AAAATATCTCACTGTCGCGCAGCAATGATTTATTAACCGAGAAATGAGAGTAAAT 417
354 CAAAGCATCTCACTGTCGCGCAGCAATGATTTATTAACCGAGCAAGTGGCACTGATTAAG 413
418 CGCGGAAATACGTCGCGCAGTGGCATGAATAGCGGCTCCGATTTGCTGATTTAGTCAGC 477
414 CGCGGAAATACGTCGCGCAGTGGCATGAATAGCTGCTGCTGATTTGCTGATTTAGTCAGC 473
478 TTTATTTGACTTAAGGGTCCCTCGTTAGTGA CAATTTGCTTTCAAGAGACAGCCATGTC 537
474 CTTATTTGACTTAAGGGTCCCTCGTTAGTGA CAATTTGCTTTCAAGAGACAGCCATGTC 533
538 CCCACACTTTGTTGAAAAACAAGTTGCTTTTGGGAAAGCACTTAAGCCACTTCTCTTC 597
534 CCCACACTTTGTTGAAAAACAAGTTGCTTTTGGGAAAGCACTTAAGCCACTTCTCTTC 593
598 AAGGAGATATTCGAGGAAAGATATTAACAGCCCTGCTGACAGCTTCTCTTGCAAA 657
594 AATAGGATCTCGAGGAGGCAATATTAACCGCTCTGCTGATTAACCTTCTTAATCCAAA 653
658 AATCAATTTGATTTCAACATATTCG--AAGACCGATGATCTACGCTTAATTTTGGTCC 715
654 AATCAATTTGATTTCAACATATTCG--AAGACCGATGATCTACGCTTAATTTTGGTCC 713
716 AACTTTGCACAGAAAGACATGACTGCGATAGCTTTTGGCCAGCAGACTGCGCTCCAGT 775
714 AACTTTGCACAGAAAGACATGACTGCGATAGCTTTTGGCCAGCAGACTGCGCTCCAGT 773
776 CCTTCGCTGATGCGCTCAATGCTGCTCAATTAACACCGGAGCGGCGACCAAC 835
774 CTTTCGCTGATGCGCTCAATGCTGCTCAATTAACACCGGAGCGGAGCGACCAAC 833
836 AGTGAAGAACTGAAGAGACGACTGCTGATACCTTTGATGATCGCCCTTTGGTAAAGG 895
834 AGTGAAGAACTGAAGAGACGAGCGCTGATACCTTTGATGATGCGCTTGGTAAAGG 893
896 TATCATTTACAGCCAGCAAGCTCATGAACGGTCAATTGGCGAGGTGCACATCAAGAGC 955
894 TATCATTTACAGCCAGCAAGCTCATGAAGGGTGAATGGGAGGTGTATTAATTATGAGGC 953
956 CAAAGGCGGGCTTATTTTGAAGGAGATCTATCTGTTGCTCAGTGCATAGGCGCAAG 1015
954 CCACGGCGGGCTTATTTTGAAGGAGATCTATCTGTTGCTCAGTGCATAGGCGCAAG 1013
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1016 TCGTATTGCAACCGGATTTTCTGTCGATATTAATGCGACAGATTAGCAGACGAGA 1075
1014 CAGTTATTGAGTGGGATTTTCTGTCGATATTAATGCGACAGATTAGCAGACGAGA 1073
1076 GAGCTCATAGAGCGTGGCCAAAGACAGAGTTAAGACAGATTTGACGCGCCCTGCAAGTCT 1135
1074 GACCTTCATGAACGTGGCCAAAGACAGAGTTAAGACAGATTTGACGCGCCCTGCAAGTCT 1133
1136 TTTATTTATCCAAAGATTGTTCACTTTGAGGAGAGCTCCGCTGAGGCCCATACTGGA 1195
1134 TTTATTTATCCAAAGATTGTTGATCTTTGAAAGAGCTCGGCTGAGGCCCATACTGGA 1193
1196 AGGATTCGATGATATCGATATGCTGCTGATTTGCTACCCGAAACGATACAGCCGA 1255
1194 AGAGATTCATGATATTCATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1253
1256 TATGCTATTGCAAGCTCGACGAGATATGAGAAATTAATTGATTCAGGATGCTCAGGA 1315
1254 TATGCTATTGCAAGCTCGACGAGATATGAGAAATTAATTGATTCAGGATGCTCAGGA 1313
1316 GTTCTTAATCCATGCGCGCTGACAGAGAAAGAAATTTCCCTTTGTCGCGCGCAGAGCTG 1375
1314 GTATCTATTCATGACGCGCGCAGAGAAAGAAATTTCCCTGAGTTAAGCAGCGCTTA 1373
1376 CGAAGCTTTGAGAGCAACATTTGCAATGATGATGATGACACAGATTTGTTTCAGAC 1435
1374 CGACGAGATTCGAAGGCTCATCCATTCGGAATGATTAATGTTGACACAGCTCCCGTCACAC 1433
1436 TTGTCGCTATTGATTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1490
1434 CTGCTTCATTTGAATTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1488

RESULT 3
US-10-363-723-2
; Sequence 2, Application US/10363723
; Publication No. US20040025205A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture Victoria Services Pty Ltd
; APPLICANT: La Trobe University
; APPLICANT: SPANGENBERG, German
; APPLICANT: LIN, Yi Han
; APPLICANT: PARISH, Roger W.
; APPLICANT: LI, Song Feng W.
; APPLICANT: HEAZLEWOOD, Joshua W.
; TITLE OF INVENTION: Manipulation of plant senescence
; FILE REFERENCE: 14403US
; CURRENT APPLICATION NUMBER: US/10/363,723
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: AU PQ9946
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: PCT/AU01/01092
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1988
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-363-723-2

Query Match 49.9%; Score 956.8; DB 8; Length 1988;
Best Local Similarity 81.4%; Pred. No. 2.4e-236;
Matches 1220; Conservative 0; Mismatches 262; Indels 16; Gaps 9;
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1 GATCCGCTTACAAGTATGCAAGTTTGTAAATTTGATATTAATGCAATCTGAGTGT 60
1 GATCCGCTTACAAGTATGCAAGTTTGTAAATTTGATATTAATGCAATCTGAGTGT 60
61 AATAAGAAATGATATGCGGTGAATATGATTTTATTTATTTATTTATTTATTTATTTAT 120
61 AATAAGAAATGATATGCGGTGAATATGATTTTATTTATTTATTTATTTATTTATTTAT 119
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QY 972 CTTGAGGAGATCTATCTCGTTGCTCAGTGCATGGCGAAAGTGTATTGGAAACGGG 1031
| | | | |
Db 1690 CTTGAGGAGAGATCTATCTCGTTGCTCAGTGCATGGCGAAAGTGTATTGGAAACGGG 1749
QY 1032 GATTTTCGTTGGCATATTATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTG 1091
| | | | |
Db 1750 GATTTTCGTTGGCATATTATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTG 1809
QY 1092 GCCAAGACCAAGATTAAAGAGATGTTAGCCCTCTGACAGTCTTTCTATTATCCAAAG 1151
| | | | |
Db 1810 GCCAAGACCAAGATTAAAGAGATGTTAGCCCTCTGACAGTCTTTCTATTATCCAAAG 1869
QY 1152 TTGGTTCACTTTGGAGGAGAGCTCGGCTGAGGCGCATACTGGAAGGATCCATGATAT 1211
| | | | |
Db 1870 TTGGTTCACTTTGGAGGAGAGCTCGGCTGAGGCGCATACTGGAAGGATCCATGATAT 1929
QY 1212 CGATATGCCCTGATATTGCTACCCAGAACAGATCAGCGCCGATATGATATGACAGCTC 1271
| | | | |
Db 1930 CGATATGCCCTGATATTGCTACCCAGAACAGATCAGCGCCGATATGCTATTGACAGCTC 1989
QY 1272 GACGAGATATGAGATTAATTTGATTCACGGTATCGCTCAGGAGTTTCTAATCCATGCG 1331
| | | | |
Db 1990 GACGAGATATGAGATTAATTTGATTCACGGTATCGCTCAGGAGTTTCTAATCCATGCG 2049
QY 1332 CGTCCAGAGAAACAGAAATTCCTTTGGTGGGCGCAGACGCTGTCCAGCGCTTTGAAGA 1391
| | | | |
Db 2050 CGTCCAGAGAAACAGAAATTCCTTTGGTGGGCGCAGACGCTGTCCAGCGCTTTGAAGA 2109
QY 1392 CCACCATTTGGAATGGA 1409
| | | | |
Db 2110 CCACCATTTGGAATGGA 2127

RESULT 5

US-11-139-461-8
; Sequence 8, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; TITLE OF INVENTION: Seeds
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Hordeum vulgare, Plant Journal 6:849-860
; OTHER INFORMATION: (1994); gene from Agrobacterium tumefaciens, Molecular
; OTHER INFORMATION: and General Genetics 216:388-394 (1989); terminator
; OTHER INFORMATION: from Zea mays, Genbank Accession #S78780.
US-11-139-461-8

Query Match 37.5%; Score 720.4; DB 13; Length 2722;
Best Local Similarity 99.9%; Pred. No. 4,6e-175;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 668 CGATGATCTACGCTCTAATTTTCGGTCCAACTTGCACAGAGAAAGATGACTGCGATG 747
| | | | |
Db 1523 CCATGATCTACGCTCTAATTTTCGGTCCAACTTGCACAGAGAAAGATGACTGCGATG 1582
QY 748 CTTTGGCCAGAGAGCTGCTCCGAGCTCTCGCTGCATGCGCGTCAATGCTGTGCTTC 807
| | | | |
Db 1583 CTTTGGCCAGAGAGCTGCTCCGAGCTCTCGCTGCATGCGCGTCAATGCTGTGCTTC 1642

QY 808 AACTATCAACCGGAAGCGGGCGACCAACAGTGGAAAGAACTGAAAGGAAGACTGCTGT 867
| | | | |
Db 1643 AACTATCAACCGGAAGCGGGCGACCAACAGTGGAAAGAACTGAAAGGAAGACTGCTGT 1702
QY 868 ACCATTGATATGCGCCCTTTGGTAAAGGATCATTTACAGCCAAAGAGCTCATGAACGGC 927
| | | | |
Db 1703 ACCATTGATATGCGCCCTTTGGTAAAGGATCATTTACAGCCAAAGAGCTCATGAACGGC 1762
QY 928 TCATTGCGAGAGTGCACAAATCAAGAGCCCAAGCGGGCTTATCTTGAAGGAGATCTA 987
| | | | |
Db 1763 TCATTGCGAGAGTGCACAAATCAAGAGCCCAAGCGGGCTTATCTTGAAGGAGATCTA 1822
QY 988 TCTCGTGTCTCAGGTGCATGCGGCAAAAGTCTTATTGAAACGGGATTTTCTGTGGCAT 1047
| | | | |
Db 1823 TCTCGTGTCTCAGGTGCATGCGGCAAAAGTCTTATTGAAACGGGATTTTCTGTGGCAT 1882
QY 1048 TTATTGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTA 1107
| | | | |
Db 1883 TTATTGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTA 1942
QY 1108 AGCAGATGTTAAGCCCTCTGACAGTCTTTCTATTATCCAAAGTGTTCACATTTGGA 1167
| | | | |
Db 1943 AGCAGATGTTAAGCCCTCTGACAGTCTTTCTATTATCCAAAGTGTTCACATTTGGA 2002
QY 1168 GGGAGCTTGGCTGAGGCGCCATTACTGGAAGGATCGATGATATGCTTGCCTCTAT 1227
| | | | |
Db 2003 GGGAGCTTGGCTGAGGCGCCATTACTGGAAGGATCGATGATATGCTTGCCTCTAT 2062
QY 1228 TTGCTAACCGAAGAACAGATCAGAGCCCGATATGCTATTTGAGCTCGACGAGATATGAGA 1287
| | | | |
Db 2063 TTGCTAACCGAAGAACAGATCAGAGCCCGATATGCTATTTGAGCTCGACGAGATATGAGA 2122
QY 1288 ATTAATTTGATTCACGATATGCTCAGAGATTTCTAATCCATGCGCTCGACAGAAACAGA 1347
| | | | |
Db 2123 ATTAATTTGATTCACGATATGCTCAGAGATTTCTAATCCATGCGCTCGACAGAAACAGA 2182
QY 1348 AATTCCTTTGGTGGGCGCGACAGCTGTGGAAGCGTTTGAAGAACCAATTTGAAATG 1407
| | | | |
Db 2183 AATTCCTTTGGTGGGCGCGACAGCTGTGGAAGCGTTTGAAGAACCAATTTGAAATG 2242
QY 1408 GA 1409
| | | | |
Db 2243 GA 2244

RESULT 6

US-11-139-461-9
; Sequence 9, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; TITLE OF INVENTION: Seeds
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648;
; OTHER INFORMATION: gene from Agrobacterium tumefaciens, Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989); terminator from Solanum
; OTHER INFORMATION: tuberosum, Plant Cell 1(1):115-122 (1989).
US-11-139-461-9

Query Match	37.5%	Score 720.4	DB 13	Length 2722
Best Local Similarity	99.9%	Pred. No. 4,66-175		
Matches 721	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	688	CGATGATCTACGTCCTAATTTTCGGTCCAACTTGCAACGAGAAACATCGACTCGATAG	747	
Db	1523	CCATGATCTACGTCCTAATTTTCGGTCCAACTTGCAACGAGAAACATCGACTCGATAG	1582	
QY	748	CTCTTGCCCGAGCACTGGCCCTCCAGTCCCTCGTGCCTGATCGGGTCCAAATGCTGTCTC	807	
Db	1583	CTCTTGCCCGAGCACTGGCCCTCCAGTCCCTCGTGCCTGATCGGGTCCAAATGCTGTCTC	1642	
QY	808	AACTATCAACCGGAGCGGGCGAACCAACATGTGAAGAACTGAAAGAAACGACTGCTGT	867	
Db	1643	AACTATCAACCGGAGCGGGCGAACCAACATGTGAAGAACTGAAAGAAACGACTGCTGT	1702	
QY	868	ACCTTGATGATCGCCCTTTGGTAAAGGATATCATTAACGCCACAGCTATGAAAGGC	927	
Db	1703	ACCTTGATGATCGCCCTTTGGTAAAGGATATCATTAACGCCACAGCTATGAAAGGC	1762	
QY	928	TCATTGGGAGAGTGCACATACGAGCGCAAGGCGGGCTTATTTCTTGAGGAGAGATCTA	987	
Db	1763	TCATTGGGAGAGTGCACATACGAGCGCAAGGCGGGCTTATTTCTTGAGGAGAGATCTA	1822	
QY	988	TCTGCTTGCTCAGGTGCATGGCGCAAGTGGTATTTGAACGCCGATTTTGTGGCATTA	1047	
Db	1823	TCTGCTTGCTCAGGTGCATGGCGCAAGTGGTATTTGAACGCCGATTTTGTGGCATTA	1882	
QY	1048	TTATTTCGCAACGAGTTTAGCAGACGAGAGAGACTTCATAGCGGTGGCCAAAGCAGAGTTA	1107	
Db	1883	TTATTTCGCAACGAGTTTAGCAGACGAGAGAGACTTCATAGCGGTGGCCAAAGCAGAGTTA	1942	
QY	1108	AGCAGATGTTACGCCCTCTGACAGTCTTTCTAATTAATCAAGAGTTGGTTCAACTTTGA	1167	
Db	1943	AGCAGATGTTACGCCCTCTGACAGTCTTTCTAATTAATCAAGAGTTGGTTCAACTTTGA	2002	
QY	1168	GGGAGCCTCGGCTBAGGCCCATATCTGAAGGAGTCGATGATTCGATATGCCCTGCTAT	1227	
Db	2003	GGGAGCCTCGGCTBAGGCCCATATCTGAAGGAGTCGATGATTCGATATGCCCTGCTAT	2062	
QY	1228	TTGCTACCCAGAAACAGATCAAGCCCGCATATGCTATTATTCAGCTCGACAGATATGAGA	1287	
Db	2063	TTGCTACCCAGAAACAGATCAAGCCCGCATATGCTATTATTCAGCTCGACAGATATGAGA	2122	
QY	1288	ATAAATTGATTCAACGGTATCGCTCAGAGTTTCTAATCATCAGCCGCTGACAGAAACGA	1347	
Db	2123	ATAAATTGATTCAACGGTATCGCTCAGAGTTTCTAATCATCAGCCGCTGACAGAAACGA	2182	
QY	1348	AATTCCTTTGGTGGCGCGACAGTGTGCAAGCGTTTGAAGAGACCACTTTGCAATGT	1407	
Db	2183	AATTCCTTTGGTGGCGCGACAGTGTGCAAGCGTTTGAAGAGACCACTTTGCAATGT	2242	
QY	1408	GA 1409		
Db	2243	GA 2244		

RESULT 7

US-11-139-461-7

Sequence 7, Application US/11139461

Publication No. US20050229274A1

GENERAL INFORMATION:

APPLICANT: Zinselmeier, Chris

APPLICANT: Haben, Jeff

APPLICANT: Tomes, Dwight

TITLE OF INVENTION: Regulated Expression of Genes in Plant

FILE REFERENCE: 0803

CURRENT APPLICATION NUMBER: US/11/139,461

CURRENT FILING DATE: 2005-05-27

PRIOR APPLICATION NUMBER: US 60/129,844

PRIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 12

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 7
; LENGTH: 5622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter and terminator from Zea mays as found in
; OTHER INFORMATION: Genbank Accession #J78780; gene from Agrobacterium
; OTHER INFORMATION: tumefaciens as found in Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989).
US-11-139-461-7

Query Match 37.5%; Score 720.4; DB 13; Length 5622;
Best Local Similarity 99.9%; Pred. No. 6,8e-175;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 688 CGATGATCTCAACGCTTAATTTGGTGCACATCTGCAGAGAAAGACATGCAGTCGCATAG 747
Db 1523 CCATGATCTCAACGCTTAATTTGGTGCACATCTGCAGAGAAAGACATGCAGTCGCATAG 1582
QY 748 CTCTTGGCCAGACAGACTGGCCCTCCAGTCCCTCGCTCGATCGCGTCAATGCTGTCTC 807
Db 1583 CTCTTGGCCAGACAGACTGGCCCTCCAGTCCCTCGCTCGATCGCGTCAATGCTGTCTC 1642
QY 808 AACTATTAACCGGAAGCGGCGACCAACATGGAAGAAGCTGAAGAAGCAAGCACTCGTGT 867
Db 1643 AACTATTAACCGGAAGCGGCGACCAACATGGAAGAAGCTGAAGAAGCAAGCACTCGTGT 1702
QY 868 ACCTTGATGATCGCCCTTTGGTAAAGGGTATCATTCAGCCAAACAGCAAGCTCATGAACGC 927
Db 1703 ACCTTGATGATCGCCCTTTGGTAAAGGGTATCATTCAGCCAAACAGCAAGCTCATGAACGC 1762
QY 928 TCATTGCGGAGGTGCACATTCAGAGGCGCAAGCGGCGCTTATTTCTTGAGGAGAGATCTA 987
Db 1763 TCATTGCGGAGGTGCACATTCAGAGGCGCAAGCGGCGCTTATTTCTTGAGGAGAGATCTA 1822
QY 988 TCTCGTGTCTCAGGTGCATGCGCGCAAGTGGTATTGGAACGGCGAATTTTCGTTGGCATTA 1047
Db 1823 TCTCGTGTCTCAGGTGCATGCGCGCAAGTGGTATTGGAACGGCGAATTTTCGTTGGCATTA 1082
QY 1048 TTATTTCCAAAGATTAGCAGACGAGAGAGCTTCATGACGCTGGCCCAAGACCAAGATT 1107
Db 1883 TTATTTCCAAAGATTAGCAGACGAGAGAGCTTCATGACGCTGGCCCAAGACCAAGATT 1942
QY 1108 AGCAGATGTTACGCCCCCTTCGCAAGTCTTTCATATACCAAGAGTGGTCAACTTTGGA 1167
Db 1943 AGCAGATGTTACGCCCCCTTCGCAAGTCTTTCATATACCAAGAGTGGTCAACTTTGGA 2002
QY 1168 GGGAGCCTCGGCTGAGGCCCATACTGGAAGGGAATCGATGATATCGATATGCCCTGTAT 1227
Db 2003 GGGAGCCTCGGCTGAGGCCCATACTGGAAGGGAATCGATGATATCGATATGCCCTGTAT 2062
QY 1228 TTGCTACCCAGAACCAATCAACGCGCGATATGCTATTGTCAGCTTCGACGCAATATGAGA 1287
Db 2063 TTGCTACCCAGAACCAATCAACGCGCGATATGCTATTGTCAGCTTCGACGCAATATGAGA 2122
QY 1288 ATAAATGATTCACGATGCGCTCAGAGAGTTTCTAATCCATGCGCGCTCGACAGGAACAGA 1347
Db 2123 ATAAATGATTCACGATGCGCTCAGAGAGTTTCTAATCCATGCGCGCTCGACAGGAACAGA 2182
QY 1348 AATTCCTTTGGTGGGCGGACAGCTGTCAAGCGTTTGAAGACCAACCATTTGAAATGT 1407
Db 2183 AATTCCTTTGGTGGGCGGACAGCTGTCAAGCGTTTGAAGACCAACCATTTGAAATGT 2242
QY 1408 GA 1409
Db 2243 GA 2244

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; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Helentjais, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(720)
US-10-409-701-2
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Query Match 37.5%; Score 720; DB 7; Length 723;

Best Local Similarity 100.0%; Pred. No. 2.8e-175;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 690 ATGATCTACGCTCTAATTTTGGTGTCCAACTTGACAGGAAAGACATCGACTGCGATAGCT 749
Db 1 ATGATCTACGCTCTAATTTTGGTGTCCAACTTGACAGGAAAGACATCGACTGCGATAGCT 60
Qy 750 CTTGCCAGACAGACTGAGCTCCCACTCTCGCTCGATCGCGTCCAAAGCTGTCTCTCA 809
Db 61 CTTGCCAGACAGACTGAGCTCCCACTCTCTGCTCGATCGCGTCCAAAGCTGTCTCTCA 120
Qy 810 CTATCAACCGGAAGCGGGGACCAACAGTGAAGAAGCTGAAGAAGCACTGCTGTAC 869
Db 121 CTATCAACCGGAAGCGGGGACCAACAGTGAAGAAGCTGAAGAAGCACTGCTGTAC 180
Qy 870 CTTGATGATCGCCCTTTTGGTAAAGGTATCATTAACCCAGCAAGCTCATGAAGGCTC 929
Db 181 CTTGATGATCGCCCTTTTGGTAAAGGTATCATTAACCCAGCAAGCTCATGAAGGCTC 240
Qy 930 ATTGGGAGGTGACAAATCAAGAGGCAAAAGCGGCTTATCTTGAAGGAGATCTATC 989
Db 241 ATTGGGAGGTGACAAATCAAGAGGCAAAAGCGGCTTATCTTGAAGGAGATCTATC 300
Qy 990 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGGCATATT 1049
Db 301 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGGCATATT 360
Qy 1050 ATTGCGAAGAGTACAGAGAGGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAG 1109
Db 361 ATTGCGAAGAGTACAGAGAGGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAG 420
Qy 1110 CAGATGTACAGCCCTCTGCAAGGTCTTCTATTATCCAAAGTGGTTCACATTTGGAGG 1169
Db 421 CAGATGTACAGCCCTCTGCAAGGTCTTCTATTATCCAAAGTGGTTCACATTTGGAGG 480
Qy 1170 GAGCTCGGCTGAGGCGCCATCTGGAAGGATCGATGATATCGATATGCCCTGTATTT 1229
Db 481 GAGCTCGGCTGAGGCGCCATCTGGAAGGATCGATGATATCGATATGCCCTGTATTT 540
Qy 1230 GCTACCCGAAACCAATCAAGCCCGCATATGCTATTGCAAGCTTCGACGAGATATGAGAT 1289
Db 541 GCTACCCGAAACCAATCAAGCCCGCATATGCTATTGCAAGCTTCGACGAGATATGAGAT 600
Qy 1290 AAATGTATTCACGATATGCTCAGAGTTTCTAATCCATGCGCGTGCAGAGAAAGAAA 1349
Db 601 AAATGTATTCACGATATGCTCAGAGTTTCTAATCCATGCGCGTGCAGAGAAAGAAA 660
Qy 1350 TTCCCTTTGGTGGGCGCAGAGCTGTCAAGAGGTTTGAAGACCAACATTTGGAATGTA 1409
Db 661 TTCCCTTTGGTGGGCGCAGAGCTGTCAAGAGGTTTGAAGACCAACATTTGGAATGTA 720
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RESULT 9

US-10-369-493-38935

; Sequence 38935, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xiandeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 38935

; LENGTH: 717

; TYPE: DNA

; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-38935

Query Match 37.4%; Score 717; DB 7; Length 717;

Best Local Similarity 100.0%; Pred. No. 1.7e-174;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 690 ATGATCTACGCTCTAATTTTGGTGTCCAACTTGACAGGAAAGACATCGACTGCGATAGCT 749
Db 1 ATGATCTACGCTCTAATTTTGGTGTCCAACTTGACAGGAAAGACATCGACTGCGATAGCT 60
Qy 750 CTTGCCAGACAGACTGAGCTCCCACTCTCGCTCGATCGCGTCCAAAGCTGTCTCTCA 809
Db 61 CTTGCCAGACAGACTGAGCTCCCACTCTCTGCTCGATCGCGTCCAAAGCTGTCTCTCA 120
Qy 810 CTATCAACCGGAAGCGGGGACCAACAGTGAAGAAGCTGAAGAAGCACTGCTGTAC 869
Db 121 CTATCAACCGGAAGCGGGGACCAACAGTGAAGAAGCTGAAGAAGCACTGCTGTAC 180
Qy 870 CTTGATGATCGCCCTTTTGGTAAAGGTATCATTAACCCAGCAAGCTCATGAAGGCTC 929
Db 181 CTTGATGATCGCCCTTTTGGTAAAGGTATCATTAACCCAGCAAGCTCATGAAGGCTC 240
Qy 930 ATTGGGAGGTGACAAATCAAGAGGCAAAAGCGGCTTATCTTGAAGGAGATCTATC 989
Db 241 ATTGGGAGGTGACAAATCAAGAGGCAAAAGCGGCTTATCTTGAAGGAGATCTATC 300
Qy 990 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGGCATATT 1049
Db 301 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGGCATATT 360
Qy 1050 ATTGCGAAGAGTACAGAGAGGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAG 1109
Db 361 ATTGCGAAGAGTACAGAGAGGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAG 420
Qy 1110 CAGATGTACAGCCCTCTGCAAGGTCTTCTATTATCCAAAGTGGTTCACATTTGGAGG 1169
Db 421 CAGATGTACAGCCCTCTGCAAGGTCTTCTATTATCCAAAGTGGTTCACATTTGGAGG 480
Qy 1170 GAGCTCGGCTGAGGCGCCATCTGGAAGGATCGATGATATCGATATGCCCTGTATTT 1229
Db 481 GAGCTCGGCTGAGGCGCCATCTGGAAGGATCGATGATATCGATATGCCCTGTATTT 540
Qy 1230 GCTACCCGAAACCAATCAAGCCCGCATATGCTATTGCAAGCTTCGACGAGATATGAGAT 1289
Db 541 GCTACCCGAAACCAATCAAGCCCGCATATGCTATTGCAAGCTTCGACGAGATATGAGAT 600
Qy 1290 AAATGTATTCACGATATGCTCAGAGTTTCTAATCCATGCGCGTGCAGAGAAAGAAA 1349
Db 601 AAATGTATTCACGATATGCTCAGAGTTTCTAATCCATGCGCGTGCAGAGAAAGAAA 660
Qy 1350 TTCCCTTTGGTGGGCGCAGAGCTGTCAAGAGGTTTGAAGACCAACATTTGGAATG 1406
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Db

661 TTCCCTTTGGTGGGCGCAGCTGTCCAGCGTTGAAGACCAACCATTCGATG 717

RESULT 10
US-10-821-711-2

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; Sequence 2, Application US/10821711
; Publication No. US20040237142a1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Blysie K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Wanggen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; FILE OF INVENTION: COMMERCIALY VIABLE TRANSGENIC PLANTS
; FILE REFERENCE: 38-21(52967) B
; CURRENT APPLICATION NUMBER: US/10/821,711
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 2
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; US-10-821-711-2

```

Query Match	30.4%	Score 583.8	DB 9	Length 723
Best Local Similarity	88.0%	Pred. No. 5.1e-140		
Matches 636	Conservative	0	Mismatches 87	Indels 0
				Gaps 0

QY 630 ATGATCTACGCTTAATTTTCGGTCCAACTGCGACAGAAAGACATCCGCTGCATAGCT 743

Db 1 ATGATCTCGCTTAATTTTCGGTCCAACTGCGACAGAAAGACGTCGACCGCGTAGCT 60

QY 750 CTTGCCACAGACTGGGCTCTCCAGTCTCTCGCTGATGGCTCCAAAGTCTGTCTCA 809
Db 61 CTTGCCACAGACTGGGCTCTCCAGTCTCTCGCTGATGGGCTCCAAAGTGTCTCTCA 120

QY	810	CTATCAACCGGAGCGGGCGACCAACAGGGAAGAACTGAAAGAAACGACTCGTCTGTAC	869
Db	121	CTGTCAACCGGAACGGAGCGACCAACAGTGGAGAACTGAAAGGAAACGAGCCGCTATAC	180

QY 870 CTTGATGATCGCCCTTTGGTAAAGGATATCATTTACAGCCAGCAAGCTCATGAAAGGGTC 923

Db 181 CTTGATGATCGCCTCTGTGGAAAGGATATCATCGACCAAGCAAGCTCATGAAAGGGTC 240

QY 930 ATTCCGGAGCTGCACATATCAGAGGCCAAAGCGCGCTTATTTCTTGAGGAGGATCTATC 989

Db 241 ATGGGGGAGCTGTATTAATTATGAGGCCACGCGCGGCTTATTTCTTGAGGAGGATCTATC 300

990 TCGTGTCTCAGGTGCATGCGCGAAGTCGATTATTGGACGCGGAAATTTTCGTTGGCAATTT 1048

1056

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QY 1050 ATTGCAACGATTGACAGCGAGAGAGCTTCATGAGCGTGCCCAAGACGAGTTAAG 11050

DB 361 ATTTGCCACGATTGACAGCGAGAGAGCTTCATGAGAGCGTGCCCAAGACGAGTTAAG 420

QY 1110 CAGATGTTACGCCCCCTCTGCAGGTCTTTCATTATCCAAAGTTGGTTCACCTTGAGG 116

D8 421 CAGATGTTACGCCCCCTCTGCAGGTCTTTCATTATCCAAAGTTGGTTCACCTTGAGG 480

QY 1170 GAGCCTCGGCTGAGCCCACTGAGAGGATCGATGATGATGCGCTGCTATTT 1222

Db 481 GAGCCTCGGCTGAGCCCACTGAGAGGATCGATGATGATGCGCTGCTATTT 540

[illegible]

QY 1290 AAATGATTCACGGTATCGCTCAGAGTTTCTAATCCATCGCGCTCGACAGAACAGAAA 134

Db 601 AAGTGAATTATGGAATCGCTCAGAGAGTATCATCATCAGCAGCGCAACAAGAGAA 660
 QY 1350 TTCCCTTTGGTGGGCGGACAGCTGTGGAAGCGTTTGAAGSACCATTTGCAATGTGA 1409
 Db 661 TTCCCTGAGATTAAACGACGCGCTTGACAGCATTTGGAAGGTATCATTCGGAATGTAT 720

QY	1410	TAG	141:
Db	721	TAG	723

RESULT 11
US-10-369

```

? Sequence 35042, Application US/10369493
? Publication No. US20030233675A1
? GENERAL INFORMATION:
? APPLICANT: Cao, Yongwei
? APPLICANT: Hinkle, Gregory J.
? APPLICANT: Slater, Steven C.
? APPLICANT: Goldman, Barry S.
? APPLICANT: Chen, Xiandeng
? TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
? FILE REFERENCE: 38-10(52052)B
? CURRENT APPLICATION NUMBER: US/10/369,493
? CURRENT FILING DATE: 2003-02-28
? PRIOR APPLICATION NUMBER: US 60/360,039
? PRIOR FILING DATE: 2002-02-21
? NUMBER OF SEQ ID NOS: 47374
? SEQ ID NO 35042
? LENGTH: 720
? TYPE: DNA
? ORGANISM: Agrobacterium tumefaciens
US-10-369-493-35042

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Query Match	30.4%	Score 583.6	DB 7	Length 720
Best Local Similarity	88.3%	Pred. No. 5.7e-140		
Matches 634	Conservative 0	Mismatches 84	Indels 0	Gaps 0

QY 690 ATGGATCTACGCTTAATTTCCGTCGCACTTCACACGGAAAGACATCGACTCGCATAGCT 749

Db 1 ATGGATCTCGCTTAATTTCCGTCGCACTTCACACGGAAAGACGCTGACCCGCGGTAGCT 60

QY 750 CTGGCCGACGACCTGGCCTCCAGTCTCTGGCTCGATCGGCTCCAAATGCTGCTCTCAA 809

Db 61 CTGGCCGACGACCTGGCCTTCAGTCTTGGCTCGATCGGCTCCAAATGTTGCTCAG 120

QY	810	CTATCAACCGGAAGCGGCGACCAACTGAAAGTAAGAAGACGCTGTCGTAC	869
Db	121	CTGTCAACCGGAGCGGAGACCAACGTGTGAAGATGAAAGGACGCGCTATATAC	180

Qy 870 CTGTGATGATCGCCCTTTGGTAAAGGGATCATATTACAGCCAAAGCACTCATGACGGCTC 929

Db 181 CTGTGATGATCGCCCTTGGTGAAGGGATCATTCGCACCCAAAGCAAGCTCATGAAAGGCTG 240

QY 930 ATTGGCGAGGTGCACAAATCAGAGGCCAAGCGGGCTATTTCCTTGAGGGAGATCTATC 989

Db 241 ATGGGGGGGGGTGTAATTAATATGAGGCCACGGGGGGCTTATTCTTGAGGGAGGATCTATC 300

Qy	990	TCGTTGCTCAGGTGCATGCGCGCAAAAGTCGTTATGTGAACGCGGATTTTCGTTGGCATATT	1049
Dh	301	TCGTTGCTCAGGTGCATGCGCGCAAAAGCATTTTGGAGTGGGATTTTCGTTGGCATATT	360

Qy 1050 ATTGCAACGAGTTAGCAGACGAGAGCTTCATGACGCGTGCCAAACACGAGTTAAG 1109

Dh 361 ATTTCGCCCTCGAGTTAGCAGACGAGAGCTTCATGAGACGTCGCGCCAAAGGCCGAGTTAAG 420

Oy 1110 CAGATGTTACGCCCTCTGCAGGCTTTCTATTATCAAGAGTGGTTCAACTTTGAGG 1169
 421 CATTCTTTTCCGCTCTGCTGCTGAGCTCTTCTATTATCCAGAGTGGTTGATCTTTTGGAAA 480

QY 1170 GAGCCCTCGAGCTGAGCCCATACCTGGAAGGATCGATGATATGCATATGCCCTGCTATTT 1229

Db 481 GAGCCTCGGCTGAGGCCACTACTGAAAGATGATGATATGCGATGTTGTT 540
Qy 1230 GCTACCCAGAACAGATCAAGCCCGATATGTAATTCAGCTCGACCGAGATATGAGAA 1289
Db 541 GCTAGCAGAACAGATCAATCCGATATGCTATTCAGCTTGAACCGAGATATGAGAT 600
Qy 1290 AAATGATTCAGGGTATGCTGCTAGAGGTTCTTAATCCATGCGGTGACAGAGAA 1349
Db 601 AAGTTGATTCATGGATGCTGCTAGAGTATCTCATCATGACGCGAGCAAGAA 660
Qy 1350 TTCCCTTTGGTGGGCGCAGCTGTGGAAGCGTTTGAAGAACACCATTTGATGT 1407
Db 661 TTCCCTCGAGTTAAGCAGACCGCTTACGAGATTGGAAGTCTCATTCGAAATGT 718

RESULT 12

US-10-369-493-38138
; Sequence 38138, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38138
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38138

Query Match 30.4%; Score 583.6; DB 7; Length 720;
Best Local Similarity 88.3%; Pred. No. 5,7e-140;
Matches 634; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 690 ATGATCTAAGCTTAATTTTGGTCCCACTTGACAGAAAGACATGCTCGATAGCT 749
Db 1 ATGATCTGCGCTAATTTTGGTCCCACTTGACAGAAAGACATGCTCGATAGCT 60
Qy 750 CTTGCGCAGCAGACGCGCTCCAGTCCCTGCTCGATCGGCTCCATGCTCTCA 809
Db 61 CTTGCGCAGCAGACGCGCTCCAGTCCCTGCTCGATCGGCTCCATGCTCTCA 120
Qy 810 CTATCAACCGAAGCGGCGCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 869
Db 121 CTGTCAACCGAAGCGGCGCAACAGTGAAGAACTGAAGAAAGCAAGCGCTGTAC 180
Qy 870 CTTGATGATCGCCCTTTGGTAAAGGTATCATTAACGCCAACAGCTCATGACGCTC 929
Db 181 CTTGATGATCGCCCTTTGGTAAAGGTATCATTAACGCCAACAGCTCATGACGCTC 240
Qy 930 ATTGGGAGGTGCAATATCAAGAGCCAAAGCGGCTTATTTCTGAGGAGATCTATC 989
Db 241 ATTGGGAGGTGTAATTAATTAAGGCCCAAGCGGCTTATTTCTGAGGAGATCTATC 300
Qy 990 TCGTGTCTCAGGTGATGAGCGCAAGTCTTATTGGAACGCGGATTTTGTGGCATATT 1049
Db 301 TCGTGTCTCAGGTGATGAGCGCAAGTCTTATTGGAACGCGGATTTTGTGGCATATT 360
Qy 1050 ATTGCAACGAGTTAGCAGACGAGAGAGCTTATGAGCGTGCACAAAGCAGAGTTAG 1109
Db 361 ATTGCAACGAGTTAGCAGACGAGAGAGCTTATGAGCGTGCACAAAGCAGAGTTAG 420
Qy 1110 CAGATGTTACGCCCTCTGAGAGTCTTTTATATTCAGAGATGTGGTTCACTTTGAGG 1169

Db 421 CAGATGTTACGCCCTCTGAGAGCTTTTATATTCAGAGATGTGGTTCACTTTGAAA 480
Qy 1170 GAGCCTCGGCTGAGGCCACTACTGAAAGGATGATGATATGATATGCGCTTAATT 1229
Db 481 GAGCCTCGGCTGAGGCCACTACTGAAAGGATGATGATATGATATGATATGCTGTTT 540
Qy 1230 GCTACCCAGAACAGATCAAGCCCGATATGTAATTCAGCTCGACCGAGATATGAGAA 1289
Db 541 GCTAGCAGAACAGATCAATCCGATATGCTATTCAGCTTGAACCGAGATATGAGAT 600
Qy 1290 AAATGATTCAGGGTATGCTGCTAGAGGTTCTTAATCCATGCGGTGACAGAGAA 1349
Db 601 AAGTTGATTCATGGATGCTGCTAGAGTATCTCATCATGACGCGAGCAAGAA 660
Qy 1350 TTCCCTTTGGTGGGCGCAGCTGTGGAAGCGTTTGAAGAACACCATTTGATGT 1407
Db 661 TTCCCTCGAGTTAAGCAGACCGCTTACGAGATTGGAAGTCTCATTCGAAATGT 718

RESULT 13

US-10-369-493-38549
; Sequence 38549, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38549
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38549

Query Match 30.4%; Score 583.6; DB 7; Length 720;
Best Local Similarity 88.3%; Pred. No. 5,7e-140;
Matches 634; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 690 ATGATCTAAGCTTAATTTTGGTCCCACTTGACAGAAAGACATGCTCGATAGCT 749
Db 1 ATGATCTGCGCTAATTTTGGTCCCACTTGACAGAAAGACATGCTCGATAGCT 60
Qy 750 CTTGCGCAGCAGACGCGCTCCAGTCCCTGCTCGATCGGCTCCATGCTCTCA 809
Db 61 CTTGCGCAGCAGACGCGCTCCAGTCCCTGCTCGATCGGCTCCATGCTCTCA 120
Qy 810 CTATCAACCGAAGCGGCGCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 869
Db 121 CTGTCAACCGAAGCGGCGCAACAGTGAAGAACTGAAGAAAGCAAGCGCTGTAC 180
Qy 870 CTTGATGATCGCCCTTTGGTAAAGGTATCATTAACGCCAACAGCTCATGACGCTC 929
Db 181 CTTGATGATCGCCCTTTGGTAAAGGTATCATTAACGCCAACAGCTCATGACGCTC 240
Qy 930 ATTGGGAGGTGCAATATCAAGAGCCAAAGCGGCTTATTTCTGAGGAGATCTATC 989
Db 241 ATTGGGAGGTGTAATTAATTAAGGCCCAAGCGGCTTATTTCTGAGGAGATCTATC 300
Qy 990 TCGTGTCTCAGGTGATGAGCGCAAGTCTTATTGGAACGCGGATTTTGTGGCATATT 1049
Db 301 TCGTGTCTCAGGTGATGAGCGCAAGTCTTATTGGAACGCGGATTTTGTGGCATATT 360
Qy 1050 ATTGCAACGAGTTAGCAGACGAGAGAGCTTATGAGCGTGCACAAAGCAGAGTTAG 1109

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Db 361 ATTGCCACGAGTTAGCAGACGAGAGACCTTCATGAACTGTGCCAAGCCAGAGTTAAG 420
Qy 1110 CAGATGTTACGCCCTCTGCGAGGTTCTTCTATTTATCCAAAGTTGGTTCAACTTTGAGG 1169
Db 421 CAGATGTTACGCCCTCTGCGAGGCTTTCTATTTATCCAAAGAGTTGGTTGATCTTTGAGAA 480
Qy 1170 GAGCTCGGCTGAGAGCCCATCTGAGAAAGGATTCGATGATGATATGATATGCTGCTATTT 1229
Db 481 GAGCTCGGCTGAGAGCCCATCTGAGAAAGATTCGATGATGATATGATATGATATGCTGCTATTT 540
Qy 1230 GCTACCCGAGAACGAGATCACGCCCGATATGCTATTCAGCTCGACGAGATATGAGAT 1289
Db 541 GCTACCCGAGAACGAGATCACATCCGATATGCTATTCAGCTTCGACGAGATATGAGAT 600
Qy 1290 AAATTGATTCACGGTATGCTCAGAGTTTCTATTCATTCATGCGCGTTCGACAGAACAGAA 1349
Db 601 AAGTTGATTCATGGGATGCTCAGAGATATCTCATTCATTCGACGCGGCAAGAACAGAA 660
Qy 1350 TTCCCTTGGTGGGCGCAGAGCTGTGAGAGGTTTGAAGACCACTTTGCAATGT 1407
Db 661 TTCCCTGAGTTAACGACGCCGCTTAGACGAGATTGAAAGTTCATTCCTTGGAAATGT 718
```

RESULT 14

```
US-11-156-084-1
; Sequence 1, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
US-11-156-084-1
```

```
Query Match 30.3%; Score 582.2; DB 16; Length 723;
Best Local Similarity 87.8%; Pred. No. 1.3e-139;
Matches 635; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
```

```
Qy 690 ATGATCTACGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCGATGACT 749
Db 1 ATGATCTGCGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCGCGGTAAGT 60
Qy 750 CTTGCCAGCAGACTGCGCTCCAGTCTCTCGCTCGATCGCGTCCAAATGCTGTCTCAA 809
Db 61 CTTGCCAGCAGACTGCGGCTTCCAGTCTCTCGCTCGATCGCGTCCAAATGTTGTCTCAG 120
Qy 810 CTATCAACCGGAAGCGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTGCTGTGAC 869
Db 121 CTGTCAACCGGAACCGGACGACCAACAGTGAAGAACTGAAAGAAAGCAAGCGCTTATAC 180
Qy 870 CTTGATATGCGCCCTTTGGTAAAGGATTCATTAAGCCAGCAAGCTCATGAACGCGCTC 929
Db 181 CTTATATATCGGCTCTGTGTGAAGGATTCATTCGACGCAAGCAAGCTCATGAAGGCTG 240
Qy 930 ATTGCGAGGTGCAATCAGAGCCCAAGGCGGCTTATTTCTTGAAGAGATCTATC 989
Db 241 ATTGCGAGGTGATTAATTAATTAAGGCCCAAGGCGGCTTATTTCTTGAAGAGATCTATC 300
Qy 990 TCGTTGCTCAGAGTGCATGCGCAAGTGTATTGGAACGCGGATTTTCTGTGCAATTT 1049
Db 301 TCGTTGCTCAGAGTGCATGCGCAAGGATTAATGAGTGTGCGGATTTTCTGTGCAATTT 360
```

```
Qy 1050 ATTGCCACGAGTTAGCAGACGAGAGAGCTTCATGAGCTGTGCCAAGCCAGAGTTAAG 1109
Db 361 ATTGCCACGAGTTAGCAGACGAGAGAGCTTCATGAGCTGTGCCAAGCCAGAGTTAAG 420
Qy 1110 CAGATGTTACGCCCTCTGCGAGGTTCTTCTATTTATCCAAAGTTGGTTCAACTTTGAGG 1169
Db 421 CAGATGTTACGCCCTCTGCGAGGCTTTCTATTTATCCAAAGAGTTGGTTGATCTTTGAGAA 480
Qy 1170 GAGCTCGGCTGAGAGCCCATCTGAGAAAGGATTCGATGATGATATGATATGCTGCTATTT 1229
Db 481 GAGCTCGGCTGAGAGCCCATCTGAGAAAGATTCGATGATGATATGATATGATATGCTGCTATTT 540
Qy 1230 GCTACCCGAGAACGAGATCACGCCCGATATGCTATTCAGCTCGACGAGATATGAGAT 1289
Db 541 GCTACCCGAGAACGAGATCACATCCGATATGCTATTCAGCTTCGACGAGATATGAGAT 600
Qy 1290 AAATTGATTCACGGTATGCTCAGAGTTTCTATTCATTCATGCGCGTTCGACAGAACAGAA 1349
Db 601 AAGTTGATTCATGGGATGCTCAGAGATATCTCATTCATTCGACGCGGCAAGAACAGAA 660
Qy 1350 TTCCCTTGGTGGGCGCAGAGCTGTGAGAGGTTTGAAGACCACTTTGCAATGTGA 1409
Db 661 TTCCCTGAGTTAACGACGCCGCTTAGACGAGATTGAAAGTTCATTCCTTGGAAATGTAT 720
Qy 1410 TAG 1412
Db 721 TAG 723
```

RESULT 15

```
US-11-156-084-20
; Sequence 20, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
US-11-156-084-20
```

```
Query Match 30.3%; Score 582.2; DB 16; Length 723;
Best Local Similarity 87.8%; Pred. No. 1.3e-139;
Matches 635; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
```

```
Qy 690 ATGATCTACGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCGATGACT 749
Db 1 ATGATCTGCGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCGCGGTAAGT 60
Qy 750 CTTGCCAGCAGACTGCGCTCCAGTCTCTCGCTCGATCGCGTCCAAATGCTGTCTCAA 809
Db 61 CTTGCCAGCAGACTGCGGCTTCCAGTCTCTCGCTCGATCGCGTCCAAATGTTGTCTCAG 120
Qy 810 CTATCAACCGGAAGCGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTGCTGTGAC 869
Db 121 CTGTCAACCGGAACCGGACGACCAACAGTGAAGAACTGAAAGAAAGCAAGCGCTTATAC 180
Qy 870 CTTGATATGCGCCCTTTGGTAAAGGATTCATTAAGCCAGCAAGCTCATGAACGCGCTC 929
Db 181 CTTATATATCGGCTCTGTGTGAAGGATTCATTCGACGCAAGCAAGCTCATGAAGGCTG 240
Qy 930 ATTGCGAGGTGCAATCAGAGCCCAAGGCGGCTTATTTCTTGAAGAGATCTATC 989
```

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Db      241 ATGGGGGGGTATATATATGAGGCCACGGGGCTTATCTTGAGGAGATCTATC 300
Qy      990 TCGTTGCTCAGGTGATGGCGGAAAGTCGTATATGGACGGGATTTTGGTCATATT 1049
Db      301 TCGTTGCTCAAGTGCATGGCGCAAGCAGTTATGGAGTGGGATTTTCTTGGCATATT 360
Qy      1050 ATTCCGACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCCAAGCCAGAGTTAAG 1109
Db      361 ATTCCGACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCCAAGCGAGTTAAG 420
Qy      1110 CAGATGTTACGGCCCTGTCAGAGTCTTCTATATCCAAAGAGTGGTTCACTTGGAGG 1169
Db      421 CAGATGTTACGGCCCTGTCAGAGCTTCTATATTCAAAGAGTGGTTGATCTTGGAAA 480
Qy      1170 GAGCCTCGGCTGAGGCCCATACCTGGAAGGATCGATGATATGATGCCCTGCTATT 1229
Db      481 GAGCCTCGGCTGAGGCCCATACCTGGAAGGATCGATGATATGATGCCCTGCTATT 540
Qy      1230 GCTACCCGAAACCAATCACGCCCGATATGCTATTGCAAGCTGACGCGAGATATGAGAA 1289
Db      541 GCTACCCGAAACCAATCACGCCCGATATGCTATTGCAAGCTGACGCGAGATATGAGAA 600
Qy      1290 AAATGATTCACGATATGCTCAGAGTTTCTATCCATGCGGCTGACAGAACAGAAA 1349
Db      601 AAATGATTCACGATATGCTCAGAGTTTCTATCCATGCGGCTGACAGAACAGAAA 660
Qy      1350 TTCCCTTGGTGGGCGCAGACAGCTGTGAAAGCGTTGAAGAACCAATTTGAAATGTA 1409
Db      661 TTCCCTTGGTGGGCGCAGACAGCTGTGAAAGCGTTGAAGAACCAATTTGAAATGTA 720
Qy      1410 TAG 1412
Db      721 TAG 723
```

Search completed: June 26, 2006, 20:38:39
Job time : 2434 secs

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QY      1521 GTTATTTTCAGTCTCTGGACGATGTTTTCAGATATATATTTGTAATAATTTGGGTTT 1580
      |||
Db      4664 GTTATTTTAAATTAATTAATAGTTAGTGTATTAATAATTAAGGCGATATATTTGGTGT 4723
QY      1581 TATATTCGTAGAAAGCAATTAATATGTAATAGTATAGCCGTTATCAAAATTTAGCAAAATTTG 1640
      |||
Db      4724 TATTAGAAAAATGCAATATTTAGAAATATATTTTAAATTAATTCCTTAAGAAAAAGAAAAAG 4783
QY      1641 TTAAGGTTCTTTTATGCGGTGAGGTTGTCACCTTTTCATCATTTGCGCGTACGAGTTA 1700
      |||
Db      4784 AAAAAATTAATTTGTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 4843
QY      1701 CGATATCCATCACTGTATGTAAGCCCGCAGAAATTTAGGGGCGCATTTAGTTT 1755
      |||
Db      4844 ATAGTTATTTTATTTTATTTTAAATGAATGTGTATTTAAAGAAATTTTATTTTATTTT 4898
```

RESULT 2

```
US-10-517-441-771
; Sequence 771, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHEIT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 771
; LENGTH: 6001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-771
```

Query Match 2.4%; Score 47; DB 6; Length 6001;

Best Local Similarity 53.6%; Pred. No. 0.0035;

Matches 98; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

```
QY      1424 TTTGTTTCAGACTTGCGCTATTGGAATAGATGTTGCTTTGTTGTTGTTGTTGTTGTT 1483
      |||
Db      1901 TTTGTAATGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1960
QY      1484 GTGATAGGCAAGTGTGGAACCTGTTTACTGGTTATTTAGTCTCTTGACG 1543
      |||
Db      1961 TTGTTATGTGTTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2020
QY      1544 ATGTTTACAAATTAATATTTGTAATATTTGTTTATTTATTTGTTAGAACGAATTAAT 1603
      |||
Db      2021 TTGATGATTTGAATGAAGGTTGTTTATATTTGTTTATTTGATGTTTATTTAAAGATTTTGA 2080
```

```
QY      1604 GGT 1606
      |||
Db      2081 GGT 2083
```

RESULT 3

```
US-10-517-441-608
; Sequence 608, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHEIT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast ce
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 608
; LENGTH: 7309
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-608
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Query Match 2.4%; Score 47; DB 6; Length 7309;

Best Local Similarity 52.9%; Pred. No. 0.0039;

Matches 101; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```
QY      1423 TTTGTTTCAGACTTGCGCTATTGGAATAGATGTTGCTTTGTTGTTGTTGTTGTTGTT 1482
      |||
Db      2840 TTATATTTTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTGTATTTTGAAGATGTTATTAATT 2899
QY      1483 TGTGATAGGCAAGTGTGGAACCTGTTTACTGGTTTATTTTACGCTCTTGAC 1542
      |||
Db      2900 TGAATTAATGAATATGCGAGAAATGTAAGTTAGTTTATTTTATTTTATTTTATTTTATTT 2959
QY      1543 GATGTTTACAAATTAATATTTGGAATTTGTTGTTTATTTATTTGTTAGAACGAATTA 1602
      |||
Db      2960 TATATTTTGAATAGTATATTTGGATATGATGAGATTTGAAGAAATTTGAGAGATGATAT 3019
QY      1603 TGTATAGTATA 1613
      |||
Db      3020 TTTTAAAGATA 3030
```

RESULT 4

```
US-10-517-441-634
; Sequence 634, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
```



```

APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almut
APPLICANT: HOFFER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast c
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 4/76-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 334
LENGTH: 7309
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-334

Query Match          2.4%; Score 45.4; DB 6; Length 7309;
Best Local Similarity 52.4%; Pred.No. 0.011;
Matches 100; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Cy      1423 TTTTGTCGACCTGGCGCATATTGAATAGATGTCGTCTTGTGTGTGTCGTCT 1482
Db      2840 TTAAATTTTGTCTTTTTTTTTTTTTTTTTTTTTCGTTTATTTGTTAGAATGTTATAACTT 2899
```

	Query Match	2.4*	Score 45.4	DB 6	Length 7309
	Best Local Similarity	52.4*	Pred. No. 0.011		
	Matches 100	Conservative 0	Mismatches 91	Indels 0	Gaps 0
OY	1423	TTTTGTTTACAGACTGTCGCTATTGTAATAAGATGTCGTCCTTGTTGTGTGGTGTG	1482		
Db	2840	TTATATTTTGTGTTTTTTTTTTTTTTTTTTTCGTTTATTTGTGTAGAAATGTTAAGTT	2899		
OY	1483	TGTGATGAGAGCAAGTGGTTGGAACCTGTTTTTACGTTATATTTCAGTCTGTGGAC	1542		
Db	2900	TGGATATTAATAGCAATATGGGAGAAATGTAAGTTAGTTTTTTTTTTTGAATTTTTTTGTT	2959		

```

QY      1483  TGTATGAGGCAAGTGGTTGGAACCTGTTTAACTGGTTATTTTCAGTCTTGAC 1542
Db      2900  TCGAATTAATGGAATAGGGAATAATGTAAGTTTAGTTTTTTTTTTACAAATTTTTCGT 2959
QY      1543  GATGTTTACCAATATATATATTGTGAAATTTGTGGTTTATATTCGTAGACGAATATA 1602
Db      2960  TATATTTTAGTAAGTATATTTGGGATAGTAGAGGTCCAGAAATTCGTAGAGATGCTAT 3019
QY      1603  TGCTAGTATA 1613
Db      3020  TTTTAAGATA 3030

RESULT 6
US-11-260-842-1
: Sequence 1, Application US/11260842
: Publication NO. US20060115845A1
: GENERAL INFORMATION:
:   APPLICANT: Vance, Jeffrey M.
:   APPLICANT: Kraus, William E.
:   APPLICANT: Goldschmidt, Pascal J.
:   APPLICANT: Gregory, Simon G.
:   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH

```

```

RESULT 6
US-11-260-842-1
; Sequence 1, Application US/11260842
; Publication No. US20060115845A1
; GENERAL INFORMATION:
; APPLICANT: Vance, Jeffrey M.
; APPLICANT: Kraus, William B.
; APPLICANT: Goldschmidt, Pascal J.
; APPLICANT: Gregory, Simon G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; FILE REFERENCE: 5405-347
; CURRENT APPLICATION NUMBER: US/11/260,842
; PRIOR FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US 60/662,447
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 261789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-260-842-1

Query Match      2.3%; Score 43.6; DB 7; Length 261789;
Match Local Similarity 51.0%; Pred. No. 0.18;
Matches 103; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

```

[illegible]

```

OY 1602 ATGTGATGATAGCCGCTATATCAAAATTAGCAAAATTTGTTAAAGCTCTT 1653
Db 1666 TTGTGAAGTTGATATATTGGGAATTGTTTATATAGATTTTTACGTTTGTCT 1717

RESULT 8
US-10-517-441-492
; Sequence 492; Application US//10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MATER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MAX, Almut
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast ce
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 492
; LENGTH: 7001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-492

Query Match 2.2%; Score 42.6; DB 6; Length 7001;
Best Local Similarity 48.5%; Pred. No. 0.063;
Matches 117; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

OY 1405 TGTGATGATTTGACCCAGTTTGTGTTGACAGTCGTGCTATTTGAATAGATGTTGCTTC 1464
Db 6641 TGGGATTAATAGATAGCAATTGGGTTTAGAATATTAGATTTTATTAATGATTTTGG 6700
OY 1465 TTGTGTGTTGTTGCTGTGTGTGATAGAGCAAGTGTTGAACCTGTTTACGCTTT 1524
Db 6701 TTTTAATTTTGGGTTTTTTTATTTGTTGTAAGTGTTGCTTTTGTATAGTTGTTT 6760
OY 1525 ATTTTCACTCTCTGGAGCAGATGTTTACAAATATATATTTGTGAATATTGGTTTTTAT 1584
Db 6761 ATTTTATATGATATTAATAGTGTTAGTAAATATTTATATGAGTAAATTTATTA 6820
OY 1585 TTGAGAGAGAAATTAATAGTAAAGTATAGCGCTTATCAAAATTTAGCAAAATTTGTTAA 1644
Db 6821 TTATTTGTGAAATTAATAAGTGAATTAATATAGTTATTTAGAAAGATGTAAAGTTTATA 6880
OY 1645 A 1645
Db 6881 A 6881

RESULT 9
US-10-517-441-766

```


US-10-517-441-538

Query Match 2.2%; Score 41.8; DB 6; Length 4316;
Best Local Similarity 45.0%; Pred. No. 0.083;
Matches 157; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 1371 GGTGCGAAGCGTTGAGGAGCACCACATTGCAATGTGATATGATGACCACTTTTGT 1430
DB |||||
QY 127 GTTGGAAGAACTTGTGATATGATGATGATGATGATGATGATGATGATGATGATG 186
DB |||||
QY 1431 CAGACTGCTGCTATTTGAAATAGAGTTCCTTTCTTTGTTGTTGTTGTTGATAG 1490
DB |||||
QY 187 GAGAGAGAGAGGTATATGTTTATGTTGTTTGTATGATGATGTTTGTGTTGTTATTA 246
DB |||||
QY 1491 AGGCAAGTGTGTTGAACTGTTTCTGTTTAACTGTTTAACTGTTTAACTGTTTAA 1550
DB |||||
QY 247 AAATGGAGATTATTTAAATGAGTTAAGTTGTTAATTTAAATATATATATATTTT 306
DB |||||
QY 1551 ACAATATATATTTGTGAAAAATGTTGTTTATTTGTTGTTGTTGTTGTTGTTGTT 1610
DB |||||
QY 307 ATTATTTAAAGATTTTAAATTTTATTTTATTTTATTTTATTTTATTTATATATA 366
DB |||||
QY 1611 ATAGCGTTATCAAAATTTAGCAAAATTTGTTAAAGTTCTTTTANCGGTGAGGTGTC 1670
DB |||||
QY 367 TATATATTTATGTTATGTTATATTAATAATATATTTATTTGTTATTTTAAAAAGATATATTT 426
DB |||||
QY 1671 GACTTTTCATCATTTGTCGCTAGAGAGTTACGATATCCATTAACGTGTA 1719
DB |||||
QY 427 TTATTTTATTTTAAATTTATGTTATGTTGTTGAGGATATAGTTGA 475
DB |||||

RESULT 14

US-10-517-441-633

; Sequence 633, Application US/10517441
; Publication No. US20060121467A1

GENERAL INFORMATION:

APPLICANT: FOEKENS, John
APPLICANT: HAREBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMIRICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
PRIOR FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 633
LENGTH: 8020
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-633

Query Match 2.2%; Score 41.8; DB 6; Length 8020;
Best Local Similarity 47.5%; Pred. No. 0.11;

Matches 124; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 1424 TTGTTCAAGCTGTGCTATTTGAAATAGATGTTGCTTTGTTGTTGTTGTTGTT 1483
DB |||||
QY 670 TTTAGTTGTTTGAATTTTGAATTTGATTTGTTAAATTTGTTTAAAGTTT 729
DB |||||
QY 1484 GTGATAGAGCAAGTGTGTTGAACTGTTTCTGTTTATTTAGTCTCTTGACG 1543
DB |||||
QY 730 GGGATTAATAGGTGGAGTATATATTTGTTTATTTAGCTTTTATTTAGTATAGAGAGAAG 789
DB |||||
QY 1544 ATGTTTCAATATATATATTTGTAATAATTTGTTGTTTATATTTGTTAGAACGAATTAAT 1603
DB |||||
QY 790 ATATTAAGTATATATTTTATTTAGTTTATTTATTTATTTTATTTTATTTATAG 849
DB |||||
QY 1604 GGTAAATAGCCCTTATCAAAATTTAGCAAAATTTGTTAAAGTTCTTTTATAGCGGTGA 1663
DB |||||
QY 850 GAAATGTTTGAAGTATATGATATGTTGATTTTGAATAATTTTGGTATGTTGA 909
DB |||||
QY 1664 GGTGTCACCTTTTCATCATTT 1684
DB |||||
QY 910 GGGTTTATGATTTTATTTTATTTT 930
DB |||||

RESULT 15

US-10-517-441-270

; Sequence 270, Application US/10517441
; Publication No. US20060121467A1

GENERAL INFORMATION:

APPLICANT: FOEKENS, John
APPLICANT: HAREBECK, Nadia
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APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast ce
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
PRIOR FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
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PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 270
LENGTH: 8169
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
NAME/KEY: unsure
LOCATION: (659, 665, 667, 668, 678, 689, 6034, 6123)
OTHER INFORMATION: unknown base
US-10-517-441-270

Query Match 2.2%; Score 41.8; DB 6; Length 8169;
Best Local Similarity 49.1%; Pred. No. 0.11;
Matches 138; Conservative 0; Mismatches 139; Indels 4; Gaps 1;

QY 1423 TTTGTTCAAGCTGTGCTATTTGAAATAGATGTTGCTTTGTTGTTGTTGTTGTT 1482
DB |||||

